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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:23:55 ; Search time 52.3019 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208
Sequence: 1 SELVEHLGNLLQANAQDQK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	208	100.0	1356	1	US-08-810-116-8
2	208	100.0	1356	1	US-07-930-548A-8
3	208	100.0	1356	2	US-09-098-707A-2
4	208	100.0	1356	2	US-09-483-539-2
5	208	100.0	1356	2	US-09-949-016-6198
6	208	100.0	1356	2	US-10-100-405A-2
7	208	100.0	1356	2	US-10-022-939-2
8	208	100.0	1456	2	US-09-949-016-9853
9	205	98.6	1367	1	US-07-813-593-4
10	205	98.6	1367	1	US-07-977-451-6
11	205	98.6	1367	1	US-07-946-507-4
12	205	98.6	1367	1	US-08-252-517-6
13	205	98.6	1367	1	US-07-906-397A-6
14	205	98.6	1367	1	US-08-601-891-6
15	205	98.6	1367	1	US-08-443-861-2
16	205	98.6	1367	1	US-09-021-324-6
17	205	98.6	1367	2	US-08-193-829B-2
18	205	98.6	1367	2	US-09-872-136B-6
19	205	98.6	1367	2	US-09-766-678-2
20	205	98.6	1367	2	US-09-919-408A-6
21	205	98.6	1367	4	PCT-US92-02750-8
22	205	98.6	1367	4	PCT-US92-05401-6
23	205	98.6	1367	4	PCT-US92-09893-6
24	101	48.6	1311	1	US-08-340-011-5
25	101	48.6	1311	2	US-08-901-710-5
26	101	48.6	1311	2	US-09-169-079-5
27	101	48.6	1338	2	US-08-750-141A-3

28	101	48.6	1338	2	US-09-119-014D-6	Sequence 6, Appli
29	89	42.8	317	2	US-09-390-326-5	Sequence 5, Appli
30	89	42.8	317	2	US-09-939-833-5	Sequence 5, Appli
31	89	42.8	317	2	US-09-506-906-5	Sequence 5, Appli
32	89	42.8	317	2	US-09-939-832-5	Sequence 5, Appli
33	89	42.8	317	2	US-09-939-754-5	Sequence 5, Appli
34	89	42.8	367	2	US-09-390-326-12	Sequence 12, Appl
35	89	42.8	367	2	US-09-939-833-12	Sequence 12, Appl
36	89	42.8	367	2	US-09-506-906-12	Sequence 12, Appl
37	89	42.8	367	2	US-09-939-832-12	Sequence 12, Appl
38	89	42.8	367	2	US-09-939-754-12	Sequence 12, Appl
39	78	37.5	294	1	US-08-701-191A-17	Sequence 17, Appl
40	78	37.5	294	2	US-09-664-526-17	Sequence 17, Appl
41	68	32.7	367	2	US-09-390-326-9	Sequence 9, Appli
42	68	32.7	367	2	US-09-939-833-9	Sequence 9, Appli
43	68	32.7	367	2	US-09-506-906-9	Sequence 9, Appli
44	68	32.7	367	2	US-09-939-832-9	Sequence 9, Appli
45	68	32.7	367	2	US-09-939-754-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-810-116-8
; Sequence 8, Application US/08810116
; Patent No. 5766860
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5766860el Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,116
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/930,548
; FILING DATE: 23-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-116-8

Query Match 100.0%; Score 208; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQDQKDYIVLPISETLSMEEDSGLSLP 42
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Query Match 100.0%; Score 208; DB 2; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 42
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 DB 1154 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 1195

RESULT 5
 US-09-949-016-6198
 ; Sequence 6198, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6198
 ; LENGTH: 1356
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6198

Query Match 100.0%; Score 208; DB 2; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 42
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 DB 1154 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 1195

RESULT 6
 US-10-100-405A-2
 ; Sequence 2, Application US/10100405A
 ; Patent No. 6841367
 ; GENERAL INFORMATION:
 ; APPLICANT: Kendall, Richard L.
 ; APPLICANT: Thomas, Kenneth A.
 ; APPLICANT: Mao, Xianzhi
 ; APPLICANT: Tebben, Andrew
 ; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
 ; FILE REFERENCE: 19963YDC
 ; CURRENT APPLICATION NUMBER: US/10/100,405A
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: 10/022,939
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/483,539
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 09/098,707
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/050,962
 ; PRIOR FILING DATE: 1997-06-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1356
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-100-405A-2

Query Match 100.0%; Score 208; DB 2; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 42
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 DB 1154 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 1195

RESULT 7
 US-10-022-939-2
 ; Sequence 2, Application US/10022939
 ; Patent No. 6841382
 ; GENERAL INFORMATION:
 ; APPLICANT: Kendall, Richard L.
 ; APPLICANT: Thomas, Kenneth A.
 ; APPLICANT: Mao, Xianzhi
 ; APPLICANT: Tebben, Andrew
 ; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
 ; FILE REFERENCE: 19963YDB
 ; CURRENT APPLICATION NUMBER: US/10/022,939
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/483,539
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 09/098,707
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/050,962
 ; PRIOR FILING DATE: 1997-06-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1356
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-022-939-2

Query Match 100.0%; Score 208; DB 2; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 42
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 DB 1154 SELVEHLGNLQANAQQDKYIVLPISETLSMEEDSGLSLP 1195

RESULT 8
 US-09-949-016-9853
 ; Sequence 9853, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9853
 ; LENGTH: 1456
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-9853

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 Best Local Similarity 100.0%; Pred. No. 3.3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
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Db 1254 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1295

RESULT 9
US-07-813-593-4
; Sequence 4, Application US/078113593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 19920415
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-813-593-4
Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
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Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193
RESULT 10
US-07-977-451-6
; Sequence 6, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-451-6
Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
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Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193
RESULT 11
US-07-946-507-4
; Sequence 4, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.

;; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
;; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
;; STREET: 180 VARICK STREET
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: U.S.A.
;; ZIP: 10014
;; COMPUTER READABLE FORM: Floppy disk
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US 07/946,507
;; FILING DATE: 19920917
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/813,593
;; FILING DATE: 24-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/793,065
;; FILING DATE: 15-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/728,913
;; FILING DATE: 28-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/679,666
;; FILING DATE: 02-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Felt, Irving N.
;; REGISTRATION NUMBER: 28,601
;; REFERENCE/DOCKET NUMBER: LEM-3-PPP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-645-1405
;; TELEFAX: 212-645-2054
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1367 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-946-507-4

Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQDGKDYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 12
US-08-252-517-6
; Sequence 6, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US 08/252,517
;; FILING DATE: 31-OCT-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,451
;; FILING DATE: 19-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/906,397
;; FILING DATE: 26-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US92/05401
;; FILING DATE: 26-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: TW 81102961
;; FILING DATE: 15-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US92/02750
;; FILING DATE: 02-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/813,593
;; FILING DATE: 24-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/793,065
;; FILING DATE: 15-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/728,913
;; FILING DATE: 28-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/679,666
;; FILING DATE: 02-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Felt, Irving N.
;; REGISTRATION NUMBER: 28,601
;; REFERENCE/DOCKET NUMBER: LEM-3-7P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-645-1405
;; TELEFAX: 212-645-2054
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1367 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-252-517-6

Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQDGKDYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 13
US-07-906-397A-6
; Sequence 6, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.

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; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/906,397A
; APPLICATION NUMBER: US/07/906,397A
; FILING DATE: 19920626
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-397A-6
;
; Query Match 98.6%; Score 205; DB 1; Length 1367;
; Best Local Similarity 97.6%; Pred. No. 8.4e-21;
; Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
; Db 1152 SELVEHLGNLQANAQQDGKDYIVLPMSSETLSMEEDSGLSLP 1193
;
; RESULT 14
; US-08-601-891-6
; Sequence 6, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,891
; FILING DATE: 15-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
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;
; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA: US 07/906,397
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-601-891-6
;
; Query Match 98.6%; Score 205; DB 1; Length 1367;
; Best Local Similarity 97.6%; Pred. No. 8.4e-21;
; Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
; Db 1152 SELVEHLGNLQANAQQDGKDYIVLPMSSETLSMEEDSGLSLP 1193
;
; RESULT 15
; US-08-443-861-2
; Sequence 2, Application US/08443861
; Patent No. 5851999
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Risau, Werner
; APPLICANT: Millauer, Birgit
; APPLICANT: Gazit, Aviv
; APPLICANT: Levitzki, Alex
; TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
; TITLE OF INVENTION: Endothelial Growth Factor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,861

FILING DATE: 22-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/193,829

FILING DATE: 09-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-060

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212)869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1367 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-443-861-2

Query Match 98.6%; Score 205; DB 1; Length 1367;

Best Local Similarity 97.6%; Pred. No. 8.4e-21;

Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1152 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 1193

Search completed: December 9, 2005, 10:35:49

Job time : 53.3019 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:20:05 ; Search time 232.189 Seconds
(without alignments)
127.621 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195
Perfect score: 208
Sequence: 1 SELVEHLGNLQNAQQDK.....IVLPISLTSMEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208	100.0	180	Q8MI23	sheep
2	208	100.0	207	Q9N112	sheep
3	208	100.0	1356	Q9N112	sheep
4	208	100.0	1451	Q9N112	sheep
5	205	98.6	341	Q8CD05	mus musculus
6	205	98.6	1343	Q5PQU0	rattus norvegicus
7	205	98.6	1343	Q5PQU0	rattus norvegicus
8	205	98.6	1345	Q8VCD0	mus musculus
9	205	98.6	1367	Q9X554	oryzotolagus
10	193	92.8	178	Q9X554	oryzotolagus
11	183	88.0	1348	Q677M1	gallus gallus
12	183	88.0	1348	Q677M1	gallus gallus
13	145	69.7	346	Q42570	xenopus laevis
14	114.5	55.0	464	Q5RIP2	brachydanio
15	114.5	55.0	829	Q5RIP2	brachydanio
16	114.5	55.0	1357	Q5GIT4	brachydanio
17	113	54.3	1328	Q4RWK3	tetraodon n
18	108	51.9	367	Q91356	coturnix co
19	108	51.9	1379	Q79701	coturnix co
20	103	49.5	1336	Q53767	rattus norvegicus
21	102	49.0	136	Q9MZE3	macaca m
22	102	49.0	1333	Q9MZE3	macaca m
23	101	48.6	453	Q9CW58	mus musculus
24	101	48.6	551	Q59GQ9	homo sapien
25	101	48.6	1338	Q5TAR1	homo sapien
26	101	48.6	1338	Q5TAR1	homo sapien
27	100	48.1	62	Q6Q2B9	scrofa
28	100	48.1	116	Q9N0K8	scrofa
29	99	47.6	86	Q8SP13	equus caball
30	99	47.6	87	Q8WMP2	equus caball
31	99	47.6	107	Q9GJZ8	callithrix

32	97	46.6	107	2	Q8MIM8	capra hircu
33	97	46.6	153	2	Q28210	bos taurus
34	97	46.6	221	2	Q9N111	ovis aries
35	91.5	44.0	1327	2	Q8QHL3	gallus gall
36	89	42.8	487	2	Q75WK4	oryzias lat
37	89	42.8	1302	1	Q6FR2	brachydanio
38	84	40.4	1331	2	Q4S572	tetraodon n
39	82	39.4	1387	2	Q4S572	tetraodon n
40	77	37.0	1272	2	Q4JDD5	brachydanio
41	77	37.0	1272	2	Q5GIT3	brachydanio
42	64	30.8	4488	2	Q9QZHI	mus musculu
43	62	29.8	323	2	Q92WY1	rhizobium m
44	62	29.8	5162	2	Q70LM6	brevibacill
45	61.5	29.6	402	2	Q4K3F2	pseudomonas

ALIGNMENTS

RESULT 1
Q8MI23 SHEEP
ID Q8MI23_SHEEP PRELIMINARY; PRT; 180 AA.
AC Q8MI23;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor receptor-2 (Fragment).
OS Ovis aries (Sheep). Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Placental artery endothelium;
RA Chung J.-Y., Tsou S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534634; AAN04105.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8MI23; 1-150.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 180 AA; 20599 MW; 70E5F444574779A0 CRC64;

Query Match 100.0%; Score 208; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQNAQQDKYIVLPISLTSMEDSGLSLP 42
Db 136 SELVEHLGNLQNAQQDKYIVLPISLTSMEDSGLSLP 177

RESULT 2
Q9N112 SHEEP
ID Q9N112_SHEEP PRELIMINARY; PRT; 207 AA.
AC Q9N112;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

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DE KDR/flk-1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Scholz T.D., Segar J.L.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233076; AAF60280.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q9N112; 1-157.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:proteinase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS01834; VEGFRECEPTR2.
DR ProDom; PD008001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
FT NON_TER 207
FT NON_TER 207
SQ SEQUENCE 207 AA; 23691 MW; 51C3950D82F988F6 CRC64;

Query Match 100.0%; Score 208; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.5e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDKYIVLPISSETLSMBEDSGSLSP 42
DB 143 SELVEHLGNLLQANAQQDKYIVLPISSETLSMBEDSGSLSP 184

RESULT 3
VGFR2 HUMAN STANDARD; PRT; 1356 AA.
ID VGR2 HUMAN STANDARD; PRT; 1356 AA.
AC P35968; O60723; Q14178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase
DE receptor Flk-1).
GN Name=KDR; Synonyms=Flk1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yin L.Y., Wu Y., Patterson C.;
RL "Full length human KDR/flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor KDR (VEGFR-2)";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 3-1356.
RC TISSUE=Umbilical vein;
RX MEDLINE=92019839; PubMed=1656371;
RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.;
RA Shows T.B.;
```

"Identification of a new endothelial cell growth factor receptor tyrosine kinase."; Oncogene 6:1677-1683(1991).

[4]

NUCLEOTIDE SEQUENCE OF 1-22. MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111; Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E., Harber E.;

"Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).

[5]

FUNCTION.

MEDLINE=93038639; PubMed=1417831; Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D., Armellino D.C., Gospodarowicz D., Boehlen P.;

"Identification of the KDR tyrosine kinase as a receptor for vascular endothelial cell growth factor."; Biochem. Biophys. Res. Commun. 187:1579-1586(1992).

-!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein kinase activity. The VEGF-kinase ligand/receptor signaling system plays a key role in vascular development and regulation of vascular permeability.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

-!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like) domains.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; AF035121; AAB88005.1; -; mRNA.

EMBL; AF063658; AAC16450.1; -; mRNA.

EMBL; X61656; CAA43837.1; -; mRNA.

EMBL; L04947; AAA59459.1; -; mRNA.

EMBL; X89776; CAA61916.1; -; Genomic_DNA.

PIR; JCI402; JCI402.

PDB; 1VR2; X-ray; A=806-1171.

Ensembl; ENSG00000128052; Homo sapiens.

HGNC; HGNC:6307; KDR.

MM; 191306; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR001824; RecepttyrknsIII.

InterPro; IPR001245; Tyr_kinase.

InterPro; IPR008266; Tyr_kinase_AS.

InterPro; IPR009134; VEGFR.

InterPro; IPR009136; VEGFR2.

PRINTS; PR01832; VEGFRECEPTR.

PRINTS; PR01834; VEGFRECEPTR2.

ProDom; PD000001; Prot_kinase; 2.

SMART; SM00408; Ig_c2; 2.

SMART; SM00219; Tyrkc; 1.

PROSITE; PS0835; IG_LIKE; 5.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

3D-structure; Angiogenesis; ATP-binding; Developmental protein; Differentiation; Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.

SIGNAL 1 19 Potential.

CHAIN	20	1356	Vascular endothelial growth factor receptor 2.
TOPO_DOM	20	764	Extracellular (Potential).
TRANSMEM	765	789	Potential.
TOPO_DOM	790	1356	Cytoplasmic (Potential).
DOMA1N	46	110	Ig-like C2-type 1.
DOMA1N	141	207	Ig-like C2-type 2.
DOMA1N	224	320	Ig-like C2-type 3.
DOMA1N	328	414	Ig-like C2-type 4.
DOMA1N	421	548	Ig-like C2-type 5.
DOMA1N	551	660	Ig-like C2-type 6.
DOMA1N	667	753	Ig-like C2-type 7.
DOMA1N	834	1162	Protein kinase.
NP_BIND	840	848	ATP (By similarity).
ACT_SITE	1028	1028	By similarity.
BINDING	868	868	ATP (By similarity).
MOD_RES	1059	1059	Phosphotyrosine (by autocatalysis) (By similarity).
CARBOHYD	46	46	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	66	66	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	96	143	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	158	158	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	245	245	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	318	318	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	374	374	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	395	395	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	511	511	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	523	523	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	580	580	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	613	613	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	619	619	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	631	631	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	675	675	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	704	704	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	721	721	N-linked (GlcNAc. . .) (Potential).
CARBOHYD	729	729	N-linked (GlcNAc. . .) (Potential).
VARIANT	472	472	V -> I (in dbSNP:2305948).
VARIANT	472	472	/FTID=VAR 022071.
CONFLICT	2	2	Q -> H (in dbSNP:1870377).
CONFLICT	772	772	/FTID=VAR 020353.
CONFLICT	787	787	Q -> E (in Ref. 2).
CONFLICT	787	787	A -> T (in Ref. 3).
CONFLICT	835	835	R -> G (in Ref. 3).
CONFLICT	848	848	K -> N (in Ref. 3).
CONFLICT	1347	1347	V -> E (in Ref. 3).
CONFLICT	1347	1347	S -> T (in Ref. 3).
SEQUENCE	1356 AA;	151527 MW;	59E7C44B05CFEBB3 CRC64;
Query Match	100.0%;	Score 208;	DB 1; Length 1356;
Best Local Similarity	100.0%;	Pred. No. 6.2e-18;	
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	SELVEHLGNLQANAQQDKDYIVLPISETLSMEEDSGLSLP 42	
DBD	1154	SELVEHLGNLQANAQQDKDYIVLPISETLSMEEDSGLSLP 1195	
RESULT 4			
Q59EB0 HUMAN			
Q59EB0 HUMAN PRELIMINARY;			PRT; 1451 AA.
IAC			
Q59EB0;			
DT	10-MAY-2005	(TrEMBLrel. 30, Created)	
DT	10-MAY-2005	(TrEMBLrel. 30, Last sequence update)	
DT	10-MAY-2005	(TrEMBLrel. 30, Last annotation update)	
DE	Kinase insert domain receptor (A type III receptor tyrosine kinase) variant (Fragment).		
DE	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;		
OC	Homo.		
OC	NCBI_TaxID=9606;		
RP	NUCLEOTIDE SEQUENCE.		
RP	(1)		

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RL  Nature 420:563-573 (2002).
RN  [4]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Thymus;
RX  MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RL  prepare full-length cDNA libraries for rapid discovery of new genes.";
RN  Genome Res. 10:1617-1630 (2000).
RP  [5]
RC  NUCLEOTIDE SEQUENCE.
RX  STRAIN=C57BL/6J; TISSUE=Thymus;
RA  Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RL  sequencing pipeline with 384 multicapillary sequencer.";
RN  Genome Res. 10:1757-1771 (2000).
RP  [6]
RC  NUCLEOTIDE SEQUENCE.
RX  STRAIN=C57BL/6J; TISSUE=Thymus;
RA  Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA  Katoh H., Kawai J., Kojima Y., Kondo S., Konno M., Koya S.,
RA  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA  Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA  Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA  Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AK031739; BAC27532.1; -; mRNA.
DR  HSSP; P35968; 1VR2.
DR  SMR; Q8CD05; 1-162.
DR  MGI; MGI:96683; Kdr.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0045165; P:cell fate commitment; IMP.
DR  GO; GO:0016477; P:cell migration; IGI.
DR  GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR  GO; GO:0030097; P:hemoiesis; IMP.
DR  GO; GO:0001570; P:vasculogenesis; IMP.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR001245; Tyr_kinase.
DR  InterPro; IPR008266; Tyr_kinase_AS.
DR  InterPro; IPR009136; VEGFR2.
DR  PRINTS; PR00109; TYRKINASE.
DR  PRINTS; PR01834; VEGFRECEPTR2.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW  Kinase. Receptor.
FT  NON_TER
SQ  SEQUENCE 341 AA; 38302 MW; EB4DCC4BB481195 CRC64;

Query Match 98.6%; Score 205; DB 2; Length 341;
Best Local Similarity 97.6%; Pred. No. 3.3e-18;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 SELVEHLGNLQANQOQKDYIVLPISSETLSMEEDSGLSLP 42
Db  148 SELVEHLGNLQANQOQKDYIVLPISSETLSMEEDSGLSLP 189

RESULT 6
VEGFR2_RAT

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ID  VEGFR2_RAT  STANDARD;  PRT;  1343 AA.
AC  O08775;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE  (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE  1).
GN  Name=Kdr; Synonyms=Flk1;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridea; Muridae; Murinae; Rattus.
OC  NCBI_TaxID=10116;
OX  [1]
RN  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Retina;
RA  Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
RL  Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC  kinase activity. The VEGF-kinase ligand/receptor signaling system
CC  plays a key role in vascular development and regulation of
CC  vascular permeability (By similarity).
CC  -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC  tyrosine phosphate.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC  receptor subfamily.
CC  -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC  domains.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; U93306; AAB97508.1; -; mRNA.
DR  EMBL; U93307; AAB97509.1; -; mRNA.
DR  HSSP; P35968; 1VR2.
DR  RGD; 2965; Kdr.
DR  GO; GO:0019838; F:growth factor binding; IMP.
DR  GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IMP.
DR  GO; GO:0048010; P:vascular endothelial growth factor receptor. .; IMP.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003598; Ig_c2.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR001824; RecepttyrkinIII.
DR  InterPro; IPR001245; Tyr_kinase.
DR  InterPro; IPR008266; Tyr_kinase_AS.
DR  InterPro; IPR009134; VEGFR.
DR  InterPro; IPR009136; VEGFR2.
DR  Pfam; PF00047; Ig; 1.
DR  PRINTS; PR01832; VEGFRECEPTOR.
DR  PRINTS; PR01834; VEGFRECEPTR2.
DR  ProDom; PD000001; Prot_kinase; 2.
DR  SMART; SM00408; IGC2; 1.
DR  SMART; SM00219; TyrKc; 1.
DR  PROSITE; PS00835; IG_LIKE; 5.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR  PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR  PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW  Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW  Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW  Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW  Tyrosine-protein kinase.
FT  SIGNAL 1 19 Potential.
FT  CHAIN 20 1343 Vascular endothelial growth factor
FT  receptor 2.
FT  TOPO_DOM 20 760 Extracellular (Potential).
FT  TRANSMEM 761 782 Potential.
FT  TOPO_DOM 783 1343 Cytoplasmic (Potential).

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FT DOMAIN          46 109 IG-like C2-type 1.
FT DOMAIN          141 207 IG-like C2-type 2.
FT DOMAIN          224 320 IG-like C2-type 3.
FT DOMAIN          328 414 IG-like C2-type 4.
FT DOMAIN          421 540 IG-like C2-type 5.
FT DOMAIN          547 654 IG-like C2-type 6.
FT DOMAIN          663 749 IG-like C2-type 7.
FT DOMAIN          830 1158 Protein kinase.
FT NP_BIND          836 844 ATP (By similarity).
FT ACT_SITE        1024 1024 By similarity.
FT BINDING         864 864 ATP (By similarity).
FT MOD_RES         1055 1055 Phosphotyrosine (by autocatalysis) (By
FT                                     similarity).
FT CARBOHYD         46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD         96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        143 143 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        158 158 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        318 318 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        395 395 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        507 507 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        576 576 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        609 609 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        615 615 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        627 627 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        671 671 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        700 700 N-linked (GlcNAc...) (Potential).
FT CARBOHYD        717 717 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE        1343 AA; 150394 MW; AD7E509EB62D3FF4 CRC64;

Query Match          98.6%; Score 205; DB 1; Length 1343;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1150 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1191

RESULT 7
Q5PQU0 RAT PRELIMINARY; PRT; 1343 AA.
AC Q5PQU0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Kdr protein.
GN Name:Kdr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hailton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Director MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087029; AAH87029.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00719; prot_kinase.
DR InterPro; IPR001824; RecepttyrkinaII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 7.
DR SMART; SM00408; IGC2; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ SEQUENCE 1343 AA; 150274 MW; F4B906E8012A5C59 CRC64;

Query Match          98.6%; Score 205; DB 2; Length 1343;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1150 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1191

RESULT 8
Q8VCD0 MOUSE PRELIMINARY; PRT; 1345 AA.
ID Q8VCD0;
AC Q8VCD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinase insert domain protein receptor.
GN Name:Kdr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020530; AAH20530.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG0000062960; Mus musculus.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1345 AA; 150460 MW; 11859F8A58A33A39 CRC64;

Query Match 98.6%; Score 205; DB 2; Length 1345;
Best Local Similarity 97.6%; Pred No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQQKQYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLLQANAQQQKQYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 9
VFGR2 MOUSE
ID VFGR2 MOUSE STANDARD; PRT; 1367 AA.
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (Kinase NYK).
GN Name=Kdr; Synonyms=Flk-1, Flk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Embryo;
RX MEDLINE=93208880; PubMed=7681362; DOI=10.1016/0092-8674(93)90573-9;
RA Millauer B., Witzigmann-Voos S., Schnurch H., Martinez R.,
RA Mueller N.P.H., Risau W., Ullrich A.;
RT "High affinity VEGF binding and developmental expression suggest Flk-1
RL as a major regulator of vasculogenesis and angiogenesis.";
RL Cell 72:835-846(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/He; TISSUE=Fetal liver;
RX MEDLINE=92020984; PubMed=1717995;
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
RA Lemiechka I.R.;
RT "A receptor tyrosine kinase cDNA isolated from a population of
RT enriched primitive hematopoietic cells and exhibiting close genetic
RT linkage to c-kit.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93141255; PubMed=8423988;
RA Celrichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.;
RT "NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from
RT E10 embryonic neuroepithelium is expressed in endothelial cells of the
RL developing embryo.";
RL Oncogene 8:11-18(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-15.
RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RL receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93361481; PubMed=8356051;
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;
RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth
RT factor and is selectively expressed in vascular endothelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung,
CC kidney, brain and skeletal muscle, but is also expressed at lower
CC levels in most other adult tissues.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X70842; CAA50192.1; -; mRNA.
DR EMBL; X59397; CAA42040.1; -; mRNA.
DR EMBL; S53103; AAB25043.1; -; mRNA.
DR EMBL; X89777; CAA61917.1; -; Genomic_DNA.
DR PIR; A41228; A41228.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG0000062960; Mus musculus.

MGI; MGI:96683; Kdr.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0045165; P:cell fate commitment; IMP.
DR GO: GO:0016477; P:cell migration; IGI.
DR GO: GO:0045446; P:endothelial cell differentiation; IDA.
DR GO: GO:0030097; P:hemopoiesis; IMP.
DR GO: GO:0001570; P:vasculogenesis; IMP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig c2.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR01824; ReceptTyrosinase.
DR InterPro: IPR01245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR009134; VEGFR.
DR InterPro: IPR009136; VEGFR2.
DR Pfam: PF00047; ig_1.
DR PRINTS: PR01832; VEGFRECEPTOR.
DR PRINTS: PR01834; VEGFRECEPTR2.
DR ProDom: PD000001; Prot_kinase; 2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00835; IG-LIKE; 5.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1367 Vascular endothelial growth factor
FT receptor 2.
FT Extracellular (Potential).
FT TOPO_DOM 20 762 Potential.
FT TRANSMEM 763 784 Cytoplasmic (Potential).
FT TOPO_DOM 785 1367 Ig-like C2-type 1.
FT DOMAIN 46 111 Ig-like C2-type 2.
FT DOMAIN 143 209 Ig-like C2-type 3.
FT DOMAIN 226 325 Ig-like C2-type 4.
FT DOMAIN 330 416 Ig-like C2-type 5.
FT DOMAIN 423 542 Ig-like C2-type 6.
FT DOMAIN 549 656 Ig-like C2-type 7.
FT DOMAIN 665 751 Protein kinase.
FT DOMAIN 832 1160 ATP (By similarity).
FT NP_BIND 838 846 By similarity.
FT ACT_SITE 1026 1026 ATP (By similarity).
FT BINDING 866 866 Phosphotyrosine (by autocatalysis) (By
FT MOD_RES 1057 similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 247 247 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 320 320 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 397 397 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 521 521 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 617 617 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 629 629 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 673 673 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 702 702 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 719 719 N-linked (GlcNAc...) (Potential).
FT CONFLICT 25 25 P -> T (in Ref. 1).
FT CONFLICT 679 679 G -> D (in Ref. 3).
FT CONFLICT 783 784 LV -> VL (in Ref. 1).
FT CONFLICT 917 917 S -> C (in Ref. 1).
FT CONFLICT 1341 1367 QLTSCLNGSGFVAPPPTGNHGRGA -> RSGPV (in
FT SEQUENCE 1367 AA; 152517 MW; EFC99704FIDCA266 CRC64;

Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 42
DB 1152 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 1193
RESULT 10
Q9XS54_RABIT PRELIMINARY; PRT; 178 AA.
AC Q9XS54;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VEGF receptor-2/Flk-1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Japanese white; TISSUE=Liver;
RA Umeki K., Kon K., Ohtaki S.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017155; BAA76520.1; -; mRNA.
DR HSSP; P35968; IVR2.
DR SMR; Q9XS54; 1-150.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 178 178
FT SEQUENCE 178 AA; 20363 MW; BSFID072A2D0A477 CRC64;
Query Match 92.8%; Score 193; DB 2; Length 178;
Best Local Similarity 92.9%; Pred. No. 5.9e-17;
Matches 39; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 42
DB 136 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 177
RESULT 11
VGFR2_COTJA STANDARD; PRT; 1348 AA.
ID VGFR2_COTJA
AC P52583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Endothelial kinase receptor EK1) (Quek 1).
GN Name:KDR; Synonyms=EK1, FLK-1;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA MEDLINE=97017121; PubMed=8863722; DOI=10.1016/0378-1119(96)00159-X;
RX Eichmann A., Marcelle C., Breat C., Le Douarin N.M.;
RT "Molecular cloning of Quak 1 and 2, two quail vascular endothelial
RL growth factor (VEGF) receptor-like molecules."; Gene 174:3-8(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 910-1348.
RC TISSUE=Spinal cord;
RA MEDLINE=93378866; PubMed=8396413; DOI=10.1016/0925-4773(93)90096-G;
RX Eichmann A., Marcelle C., Breat C., Le Douarin N.M.;
RA "Two molecules related to the VEGF receptor are expressed in early
RT endothelial cells during avian embryonic development."; Mech. Dev. 42:33-48(1993).
RL [3]
RP NUCLEOTIDE SEQUENCE OF 764-880, AND CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909; DOI=10.1006/dbio.1995.1180;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1)
RL are expressed during vasculogenesis and vascular differentiation in
RN the quail embryo."; Dev. Biol. 169:699-712(1995).
RP NUCLEOTIDE SEQUENCE OF 1023-1079.
RC PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RL the avian embryo."; Oncogene 7:2479-2487(1992).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In all endothelial tissues during onset of
CC vascularization. In later development, present in lung, heart,
CC intestine and skin.
CC -!- DEVELOPMENTAL STAGE: Expressed in whole mesoderm at onset of
CC gastrulation. From day 2, confined to endothelial tissues and
CC expression continues to be widespread throughout vascularization
CC until E9 where it becomes restricted to specific regions such as
CC the spinal chord and heart valves.
CC -!- INDUCTION: In vitro, it is induced by basic fibroblast growth
CC factor (bFGF), uniquely in the first 24 hours of cell culture.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X83288; CAA58268.1; -; mRNA.
CC EMBL; S65205; AAB28127.1; -; mRNA.
CC EMBL; S78345; AAB34594.1; -; mRNA.
CC PIR; JC4953; S51656.
CC HSSP; P35968; 1VR2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig C2.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001824; Receptor_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase.
CC InterPro; IPR009134; VEGFR.
CC InterPro; IPR009136; VEGFR2.
CC Pfam; PF00047; Ig; 1.

DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR PRODOM; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Phosphorylation; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphoprotein; Phosphotyrosine; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 1348 Vascular endothelial growth factor
FT receptor 2.
FT Extracellular (Potential).
FT Potential.
FT Cytoplasmic (Potential).
FT IG-like C2-type 1.
FT IG-like C2-type 2.
FT IG-like C2-type 3.
FT IG-like C2-type 4.
FT IG-like C2-type 5.
FT IG-like C2-type 6.
FT IG-like C2-type 7.
FT DOMAIN 658 744 Protein kinase.
FT DOMAIN 825 1155 ATP (By similarity).
FT NP BIND 831 839 By similarity.
FT ACT SITE 1021 1021 ATP (By similarity).
FT BINDING 859 859 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 153 153 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 240 240 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 386 386 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 556 556 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 603 603 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 613 613 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 666 666 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 688 688 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 710 710 N-linked (GlcNAc...) (Potential).
FT CONFLICT 865 865 A -> S (in Ref. 3).
SQ SEQUENCE 1348 AA; 150306 MW; A5B419A76FD5FB3 CRC64;
Query Match 88.08; Score 183; DB 1; Length 1348;
Best Local Similarity 83.38; Pred No. 1.2e-14;
Matches 35; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SELVHGLNLIQANAOQDKDYIVLPISETLSMEEDSGLSLP 42
Db 1147 SELVHGLNLIQANVQDKDYVVLPLSVLSINMEEDSGLSLP 1188
RESULT 12
Q677M1_CHICK
ID Q677M1_CHICK PRELIMINARY; PRT; 1348 AA.
AC Q677M1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Vascular endothelial growth factor receptor 2.
GN Name=Flk1;
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hashimoto T.;
RT "Modulation of retinal neurogenesis by vascular endothelial growth factor";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY382882; AAR26285.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PRO1832; VEGFRECEPTOR.
DR PRINTS; PRO1834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 7.
DR SMART; SM00408; IGc2; 5.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Receptor.
SQ SEQUENCE 1348 AA; 150121 MW; F6EFOF21CA839D6E CRC64;

Query Match 88.0%; Score 183; DB 2; Length 1348;
Best Local Similarity 83.3%; Pred. No. 1.2e-14;
Matches 35; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1147 SELVEHLGNLQANVRQDGKDYIVLPISVLSNMEEDSGLSLP 1198

RESULT 13
O42570 XENLA
ID O42570 XENLA PRELIMINARY; PRT; 346 AA.
AC O42570;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase (Fragment).
GN Name=flk-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;

RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT "Neovascularization of the Xenopus embryo";
RL Dev. Dyn. 0:0-0(1997).
DR EMBL; AF007760; AAB63281.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; O42570; 1-164.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PRO109; TYRKINASE.
DR PRINTS; PRO1834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase; Receptor.
FT NON_TER 1 346
FT NON_TER 346
SQ SEQUENCE 346 AA; 38976 MW; AA35FA8F0C702416 CRC64;

Query Match 69.7%; Score 145; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 2.5e-10;
Matches 28; Conservative 10; Mismatches 2; Indels 2; Gaps 1;

OY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 150 SELVEHLGNLQASAHQDGKDYI--PLTVSLNIEDDSGVSM 189

RESULT 14
Q5RIP2 BRARE
ID Q5RIP2 BRARE PRELIMINARY; PRT; 464 AA.
AC Q5RIP2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to vertebrate kinase insert domain receptor (A type III receptor tyrosine kinase) (KDR) (Fragment).
GN Name=OTTDARP0000004701; ORFNames=BUSM1-205D10.1-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248242; CA11526.1; -; Genomic DNA.
DR Ensembl; ENSDARG00000017321; Danio rerio.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor; Transferase.
FT NON_TER 1 464
FT NON_TER 464 464
SQ SEQUENCE 464 AA; 52430 MW; FA84BBA573F7DC88 CRC64;

Query Match 55.0%; Score 114.5; DB 2; Length 464;
Best Local Similarity 69.4%; Pred. No. 3.5e-06;
Matches 25; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SELVEHLGNLLQANAQDGKDYIVLPISFSLMEED 36
Db 400 TQLVEHLGNLLQASAQDGKDYIPLTNGE---MEEE 432

RESULT 15
Q5TZ34 BRARE
ID Q5TZ34 BRARE PRELIMINARY; PRT; 829 AA.
AC Q5TZ34;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel kinase insert domain receptor protein (Fragment).
GN Name=OTTDARP0000004831; ORFNames=CH211-254J6.1-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OK NCBI_taxid=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX511058; CAH68950.1; -; Genomic DNA.
DR Ensembl; ENSDARG00000017321; Danio rerio.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR002290; Ser thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Receptor; Transferase; Transmembrane.
FT NON_TER 1 829
FT NON_TER 829 829
SQ SEQUENCE 829 AA; 92982 MW; 6FFAE9BD19856F51 CRC64;

Query Match 55.0%; Score 114.5; DB 2; Length 829;
Best Local Similarity 69.4%; Pred. No. 6.7e-06;
Matches 25; Conservative 4; Mismatches 4; Indels 3; Gaps 1;
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Qy 1 SELVEHLGNLLQANAQDGKDYIVLPISFSLMEED 36
Db 645 TQLVEHLGNLLQASAQDGKDYIPLTNGE---MEEE 677

Search completed: December 9, 2005, 10:33:47
Job time : 234.189 secs
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:21:00 ; Search time 36.4528 Seconds
(without alignments)
110.858 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208
Sequence: 1 SELVEHLGNLQANAQQDK.....IVLPISLTSMEDSGLSLP 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	1356	JC1402	protein-tyrosine k
2	205	98.6	1367	A41228	protein-tyrosine k
3	183	88.0	1348	S51656	vascular endotheli
4	108	51.9	1367	B56598	endothelial kinase
5	108	51.9	1379	JC4954	vascular endotheli
6	103	49.5	1330	S49010	embryonic receptor
7	103	49.5	1336	I60598	Fit-1 tyrosine kin
8	102	49.0	1333	I78875	receptor tyrosine
9	101	48.6	1338	S09982	protein-tyrosine k
10	62	29.8	323	E95864	probable ABC trans
11	60	28.8	334	F71480	probable flagellar
12	60	28.8	450	S42825	serum response fac
13	59.5	28.6	1288	A48999	protein-tyrosine k
14	59	28.4	186	D83083	probable two-compo
15	59	28.4	595	JC6550	sex-determining re
16	57.5	27.6	175	C70453	translation initia
17	57.5	27.6	903	F82080	preprotein translo
18	57.5	27.6	1018	T30853	antigenic heat-sta
19	56.5	27.2	859	T35785	probable beta-gluc
20	55	26.4	286	T21545	hypothetical prote
21	55	26.4	323	AH3187	nitrotriacetate
22	55	26.4	372	T28027	hypothetical prote
23	55	26.4	1663	C3HU	complement C3 prec
24	54.5	26.2	1058	T19282	hypothetical prote
25	54	26.0	109	AD1600	B. subtilis YnaA p
26	54	26.0	160	B89841	hypothetical prote
27	54	26.0	906	AD3267	protein translocas
28	54	26.0	1118	1 SYBYCP	carbamoyl-phosphat
29	53.5	25.7	470	S71466	homeotic protein S

30	53.5	25.7	627	2	B83692	hypothetical prote
31	53.5	25.7	799	2	T00052	hypothetical prote
32	52.5	25.2	619	2	F82387	hypothetical prote
33	52.5	25.2	1026	2	C97783	cell surface antig
34	52.5	25.2	1363	2	I58375	protein-tyrosine k
35	52.5	25.2	1630	2	T40217	hypothetical prote
36	52	25.0	332	2	F81743	conserved hypothet
37	52	25.0	340	2	A10195	DNA-directed DNA p
38	52	25.0	534	2	B96642	hypothetical prote
39	52	25.0	623	2	T16384	hypothetical prote
40	52	25.0	1026	2	T05882	hypothetical prote
41	51.5	24.8	413	2	E70177	acetate kinase (ac
42	51.5	24.8	612	2	E84809	hypothetical prote
43	51.5	24.8	864	2	S60441	hypothetical prote
44	51.5	24.8	1066	2	S50237	TATA box-binding p
45	51.5	24.8	2004	2	T30185	hypothetical prote

ALIGNMENTS

RESULT 1

JC1402
protein-tyrosine kinase (EC 2.7.1.112) KDR - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 05-Oct-2004
C:Accession: JC1402; I58357
R:Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gosp
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A:Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelial
A:Reference number: JC1402; MUID:93038639; PMID:1417831
A:Accession: JC1402
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-616, 'E', 618-700, 'E', 702-748, 'F', 750-1263, 'I', 1265-1290, 'P', 1292-
A:Cross-references: UNIPROT:F35988; UNIPARC:UPI000017A3C3; EMBL:X61656; NID:931717
R:Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.
Oncogene 6, 1677-1683, 1991
A:Title: Identification of a new endothelial cell growth factor receptor tyrosine kinase
A:Reference number: I58357; MUID:92019839; PMID:1656371
A:Accession: I58357
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 3-1356 <TER2>
A:Cross-references: UNIPARC:UPI000016A991; GB:I04947; NID:G186674; PIDN:AAA59459.1; PID
A:Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.
C:Genetics:
A:Gene: GDB:KDR
A:Cross-references: GDB:127921; OMIM:191306
A:Map position: 4q12-4q12
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
F;766-790/Domain: transmembrane #status predicted <TM>
F;832-1167/Domain: protein kinase homology <KIN>
F;840-848/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDKYIVLPISLTSMEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLQANAQQDKYIVLPISLTSMEDSGLSLP 1195

RESULT 2

A41228
protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C:Species: Mus musculus (house mouse)
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
R:Accession: A41228; A46065; I58365; S18832; S29991
C:Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A:Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primiti

RESULT 8
I78875
receptor tyrosine kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence revision
02-Aug-1996 #text change 05-Oct-2004

A:Accession: E35804
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <KUR>

A:Cross-references: UNIPROT:Q92WY1; UNIPARC:UPI00000CB441; GB:AL591985; PIDN:CAC48581.1.1									
A:Experimental source: strain 1021, megaplasmid pSymB									
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, J.;									
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;									
L.; Hyman, R.W.; Jones, T.									
Science 293, 668-672, 2001									
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,									
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.									
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.									
A:Reference number: A96039; MUID:21368234; PMID:11474104									
A:Contents: annotation									
C:Genetics:									
A:Gene: SMB20181									
A:Genome: plasmid									
Query Match 29.8%; Score 62; DB 2; Length 323;									
Best Local Similarity 41.2%; Pred. No. 2.8;									
Matches 14; Conservative 8; Mismatches 8; Indels 4; Gaps 2;									
Qy	13	ANAAQDGKDYIVLPISET---LSNEEDSGL-SLP 42							
Db	89	ANQRASGKDYFIPYRAVGGLMKDPSGIKALP 122							
: : : : : :									
RESULT 11									
F71480									
probable flagellar m-ring protein - Chlamydia trachomatis (serotype D, strain UW3/Cx)									
C:Species: Chlamydia trachomatis									
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004									
C:Accession: F71480									
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,									
Science 282, 754-759, 1998									
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach									
A:Reference number: A71570; MUID:99000809; PMID:9784136									
A:Accession: F71480									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-334 <ARN>									
A:Cross-references: UNIPROT:O84724; UNIPARC:UPI00000D338F; GB:AE001342; GB:AE001273; NID									
A:Experimental source: serotype D, strain UW-3/Cx									
C:Genetics:									
A:Gene: flfF									
Query Match 28.8%; Score 60; DB 2; Length 334;									
Best Local Similarity 41.5%; Pred. No. 5.2;									
Matches 22; Conservative 4; Mismatches 13; Indels 14; Gaps 3;									
Qy	4	VEHLGNL----LQANAQDGKDYI---VLPISETLSMEEDS-----GLSLP 42							
Db	57	LSHLGNLQSIIEIQAKKEQKDLTFEPVLQATVLSQEEDSLAEISVILSLP 109							
: : : : :									
RESULT 12									
S42825									
serum response factor homolog - fruit fly (Drosophila melanogaster)									
C:Species: Drosophila melanogaster									
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004									
C:Accession: S42825									
R:Groppe, J.C.									
submitted to the EMBL Data Library, February 1994									
A:Reference number: S42825									
A:Accession: S42825									
A:Status: preliminary									
A:Molecule type: mRNA									
A:Residues: 1-450 <GRO>									
A:Cross-references: UNIPROT:Q24535; UNIPARC:UPI0000135F3A; EMBL:X77532; NID:G453586; PID									
C:Genetics:									
A:Gene: FlyBase:Serf									
A:Cross-references: FlyBase:FBgn0010354									
F:166-221/Domain: serum response factor DNA-binding domain homology <SRF>									
Query Match 28.8%; Score 60; DB 2; Length 450;									
Best Local Similarity 45.0%; Pred. No. 7.3;									

Matches	9;	Conservative	6;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	11	LQANAQODGKDYIVLPISET 30							
Db	390	LQVHAEDGNQYVITPLSST 409							
RESULT 13									
A48999									
protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human									
N:Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase 4									
C:Species: Homo sapiens (man)									
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004									
C:Accession: A48999; A44930; G02316; S36130; A42010									
R:Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Alitalo, R.;									
Cancer Res. 52, 5738-5743, 1992									
A:Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops									
A:Reference number: A48999; MUID:93007958; PMID:1327515									
A:Accession: A48999									
A:Status: preliminary; not compared with conceptual translation									
A:Molecule type: mRNA									
A:Residues: 1-1298 <PAJ>									
A:Cross-references: UNIPROT:P35916; UNIPARC:UPI0000138777; PIDN:AAB23636.1; PID:									
A:Experimental source: HEL erythroleukemia cells									
A:Note: sequence extracted from NCBI backbone (NCBIP:115335)									
R:Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo, R.; Baile									
Cancer Res. 52, 746-748, 1992									
A:Title: FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-q									
A:Reference number: A44930; MUID:92119639; PMID:1310071									
A:Accession: A44930									
A:Status: preliminary; not compared with conceptual translation									
A:Molecule type: mRNA									
A:Residues: 761-1190 <APR>									
A:Cross-references: UNIPARC:UPI000017A3EA; GB:X68203; NID:G31433									
A:Note: sequence extracted from NCBI backbone (NCBIP:78155)									
R:Wood, W.I.									
submitted to the EMBL Data Library, December 1995									
A:Reference number: H01039									
A:Accession: G02316									
A:Status: translated from GB/EMBL/DBJ									
A:Molecule type: mRNA									
A:Residues: 1-1298 <WOO>									
A:Cross-references: UNIPARC:UPI0000138777; EMBL:U43143; NID:G1150990; PIDN:AAA8									
R:Galland, F.									
submitted to the EMBL Data Library, December 1992									
A:Reference number: S36130									
A:Accession: S36130									
A:Molecule type: mRNA									
A:Residues: 1-23,'D',25-744,'P',746-751,'RP',754-889,'Q',891-1127,'V',1129-1145,'									
A:Cross-references: UNIPARC:UPI00003CA99; EMBL:X69878; NID:G297049; PIDN:CAA49									
R:Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnba									
Genomics 13, 475-478, 1992									
A:Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase									
A:Reference number: A42010; MUID:92307693; PMID:1319394									
A:Accession: A42010									
A:Status: preliminary; nucleic acid sequence not shown; not compared with conce									
A:Molecule type: mRNA									
A:Residues: 776-889,'Q',891-1127,'V',1129-1145,'H',1147-1163,'D',1165-1200 <GAL									
A:Cross-references: UNIPARC:UPI000017A3EB									
C:Genetics:									
A:Gene: GDB:FLT4									
A:Cross-references: GDB:128732; OMIM:136352									
A:Map position: 5q34-5q35									
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; trans									
F:1-23/Domain: signal sequence #status predicted <SIG>									
F:24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>									
F:843-1176/Domain: protein kinase homology <KIN>									
F:851-859/Region: protein kinase ATP-binding motif									
Query Match 28.6%; Score 59.5; DB 2; Length 1298;									
Best Local Similarity 45.9%; Pred. No. 28;									
Matches 17; Conservative 6; Mismatches 13; Indels 1; Gaps 1;									

QY 1 SELVEHLGNLQNAQQDGKDYIVLPISETLSMEEDS 37
 ||||| ||||| : : : : :
 Db 1163 SELVEILGDLQGRGLQBEVEVCMAPRS-SQSSEGS 1198

RESULT 14

D83083
 probable two-component response regulator PA4493 [imported] - Pseudomonas aeruginosa (sp
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Jun-2003
 C:Accession: D83083
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: D83083
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <STO>
 A:Cross-references: UNIPARC:UPI00000C5D35; GB:AE004863; GB:AE004091; NID:9950731; PIDN:
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4493
 C:Superfamily: response regulator, RegA/PrrA/ActR type; response regulator homology

Query Match 28.4%; Score 59; DB 2; Length 186;
 Best Local Similarity 58.6%; Pred. No. 3.6;
 Matches 17; Conservative 0; Mismatches 8; Indels 4; Gaps 1;

QY 13 ANAQDQGDYIVLPISETLSMEEDSGLSL 41
 ||||| ||||| ||||| |||||
 Db 50 ALAQDTPDYAVL----DLKMGDSGLVL 74

RESULT 15

JC6550
 sex-determining region Y gene-related protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 15-Mar-2004
 C:Accession: JC6550
 R:Kido, S.; Hiraoka, Y.; Ogawa, M.; Sakai, Y.; Yoshimura, Y.; Aiso, S.
 Gene 208, 201-206, 1998
 A:Title: Cloning and characterization of mouse mSox13 cDNA.
 A:Reference number: JC6550; MUID:98201614; PMID:9524265
 A:Accession: JC6550
 A:Molecule type: mRNA
 A:Residues: 1-595 <KID>
 A:Cross-references: UNIPARC:UPI000016C745; DDBJ:AB006329; NID:93077735; PIDN:BAA25786.1;
 A:Experimental source: embryo
 C:Comment: This protein is capable of binding the AACAAT sequence.
 C:Genetics:
 A:Gene: sox13
 C:Keywords: embryo; leucine zipper
 F:395-470/Domain: HMG box homology <HMG1>

Query Match 28.4%; Score 59; DB 2; Length 595;
 Best Local Similarity 35.7%; Pred. No. 14;
 Matches 15; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 5 EHLGNLQNAQQDGKDYIVLP-----SETLSMEEDSGLSLP 42
 :||| ||||| ||||| ||||| : : : : :
 Db 184 QHKINLQQOIQVNNPYPVMPFPPSHQPLVTPDPSQLALP 225

Search completed: December 9, 2005, 10:34:39
 Job time : 38.4528 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 11:21:30 ; Search time 63 Seconds
(without alignments)
278.553 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195
Perfect score: 208
Sequence: 1 SELVEHLGNLQNAQQDGK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
5: /cn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
6: /cn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208	100.0	429	US-10-664-421-44	Sequence 44, Appl
2	208	100.0	429	US-10-941-635-44	Sequence 44, Appl
3	208	100.0	567	US-10-327-414-8	Sequence 8, Appl
4	208	100.0	1306	US-10-741-600-1470	Sequence 1470, Ap
5	208	100.0	1354	US-10-262-538-30	Sequence 30, Appl
6	208	100.0	1354	US-10-669-176-30	Sequence 30, Appl
7	208	100.0	1356	US-09-969-037-7	Sequence 7, Appl
8	208	100.0	1356	US-10-022-939-2	Sequence 2, Appl
9	208	100.0	1356	US-10-100-405A-2	Sequence 2, Appl
10	208	100.0	1356	US-10-327-414-6	Sequence 6, Appl
11	208	100.0	1356	US-10-090-183-2	Sequence 2, Appl
12	208	100.0	1356	US-10-165-193A-11	Sequence 11, Appl
13	208	100.0	1356	US-10-394-322A-66	Sequence 66, Appl
14	208	100.0	1356	US-10-440-464-129	Sequence 129, App
15	208	100.0	1356	US-10-783-528-61	Sequence 61, Appl
16	208	100.0	1356	US-10-872-198-115	Sequence 115, App
17	208	100.0	1356	US-10-763-276-7	Sequence 7, Appl
18	208	100.0	1356	US-10-741-600-1469	Sequence 1469, Ap
19	208	100.0	1356	US-10-741-600-1471	Sequence 1471, Ap
20	208	100.0	1356	US-10-926-806-10	Sequence 10, Appl
21	208	100.0	1356	US-10-824-982-2	Sequence 2, Appl
22	208	100.0	1356	US-11-021-951-115	Sequence 115, App
23	205	98.6	1345	US-10-090-183-6	Sequence 6, Appl
24	205	98.6	1367	US-09-919-408-6	Sequence 6, Appl
25	205	98.6	1367	US-09-766-678-2	Sequence 2, Appl
26	205	98.6	1367	US-09-872-136-6	Sequence 6, Appl
27	205	98.6	1367	US-10-165-193A-10	Sequence 10, Appl

28	205	98.6	1367	5	US-10-639-603-6	Sequence 6, Appli
29	205	98.6	1367	5	US-10-799-782-2	Sequence 2, Appli
30	205	98.6	1367	6	US-11-030-539-6	Sequence 6, Appli
31	102	49.0	1333	4	US-10-394-322A-65	Sequence 65, Appl
32	101	48.6	1311	3	US-09-765-534B-5	Sequence 5, Appli
33	101	48.6	1311	4	US-10-774-802-5	Sequence 5, Appli
34	101	48.6	1338	4	US-10-060-065-23	Sequence 23, Appl
35	101	48.6	1338	4	US-10-059-585-44	Sequence 44, Appl
36	101	48.6	1338	4	US-10-021-660-84	Sequence 84, Appli
37	101	48.6	1338	4	US-10-090-183-4	Sequence 4, Appli
38	101	48.6	1338	4	US-10-116-275-139	Sequence 129, App
39	101	48.6	1338	4	US-10-211-462-215	Sequence 215, App
40	101	48.6	1338	4	US-10-621-116-26	Sequence 26, Appl
41	101	48.6	1338	5	US-10-872-198-114	Sequence 114, App
42	101	48.6	1338	5	US-10-926-806-8	Sequence 8, Appli
43	101	48.6	1338	5	US-10-824-982-4	Sequence 4, Appli
44	101	48.6	1338	6	US-11-021-951-114	Sequence 114, App
45	101	48.6	1339	4	US-10-165-193A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-664-421-44
; Sequence 44, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIVAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-44

Query Match 100.0%; Score 208; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQNAQQDGKQYIVLPISETLSMEEDSGLSLP 42
DB 371 SELVEHLGNLQNAQQDGKQYIVLPISETLSMEEDSGLSLP 412

RESULT 2
US-10-941-635-44
; Sequence 44, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15

; PRIOR APPLICATION NUMBER: 60/503,277
 ; PRIOR FILING DATE: 2003-09-15
 ; NUMBER OF SEQ ID NOS: 167
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 44
 ; LENGTH: 429
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Mammalian
 ; OTHER INFORMATION: protein sequence
 US-10-941-635-44

 Query Match 100.0%; Score 208; DB 5; Length 429;
 Best Local Similarity 100.0%; Pred. No. 5.1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 Db 371 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 412

 RESULT 3
 US-10-327-414-8
 ; Sequence 8, Application US/10327414
 ; Publication No. US20030158083A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Peters, Kevin G
 ; TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Function of
 ; TITLE OF INVENTION: Endothelia Phosphatase
 ; FILE REFERENCE: 8864M
 ; CURRENT APPLICATION NUMBER: US/10/327,414
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/355,125
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 567
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-327-414-8

 Query Match 100.0%; Score 208; DB 4; Length 567;
 Best Local Similarity 100.0%; Pred. No. 7.2e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 Db 365 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 406

 RESULT 4
 US-10-741-600-1470
 ; Sequence 1470, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1470
 ; LENGTH: 1306
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-741-600-1470

 Query Match 100.0%; Score 208; DB 5; Length 1306;

 Best Local Similarity 100.0%; Pred. No. 2.1e-19;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 Db 1104 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1145

 RESULT 5
 US-10-262-538-30
 ; Sequence 30, Application US/10262538
 ; Publication No. US20030113324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo et al
 ; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
 ; FILE REFERENCE: 28967/37564
 ; CURRENT APPLICATION NUMBER: US/10/262,538
 ; CURRENT FILING DATE: 2002-09-30
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 1354
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-262-538-30

 Query Match 100.0%; Score 208; DB 4; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 2.2e-19;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 Db 1152 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

 RESULT 6
 US-10-669-176-30
 ; Sequence 30, Application US/10669176
 ; Publication No. US20040214766A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo et al
 ; TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR TREATMENT OF
 ; TITLE OF INVENTION: NEUROPATHOLOGIES
 ; FILE REFERENCE: 28967/37564B
 ; CURRENT APPLICATION NUMBER: US/10/669,176
 ; CURRENT FILING DATE: 2003-09-23
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 1354
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-669-176-30

 Query Match 100.0%; Score 208; DB 4; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 2.2e-19;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 Db 1152 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

 RESULT 7
 US-09-969-037-7
 ; Sequence 7, Application US/09969037
 ; Publication No. US2003002247A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
 ; TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
 ; TITLE OF INVENTION: for 1175-tyrosine phosphorylated KDR/Flk-1 and usages of the same
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/969,037

; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-09-969-037-7

Query Match 100.0%; Score 208; DB 3; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 1195

RESULT 8

US-10-022-939-2
; Sequence 2, Application US/10022939
; Publication No. US20030032160A1
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 1195

RESULT 9

US-10-100-405A-2
; Sequence 2, Application US/10100405A
; Publication No. US20030055239A1
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDC
; CURRENT APPLICATION NUMBER: US/10/100,405A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/022,939
; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-100-405A-2

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 1195

RESULT 10

US-10-327-414-6
; Sequence 6, Application US/10327414
; Publication No. US20030158083A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin G
; TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Function of
; TITLE OF INVENTION: Endothelial Phosphatase
; FILE REFERENCE: 8864M
; CURRENT APPLICATION NUMBER: US/10/327,414
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/355,125
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-414-6

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGSLP 1195

RESULT 11

US-10-090-183-2
; Sequence 2, Application US/10090183
; Publication No. US20030185802A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ralph A. Reisfeld
; APPLICANT: Andrew G. Niethammer
; APPLICANT: Rong Xiang
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-829.0
; CURRENT APPLICATION NUMBER: US/10/090,183
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT

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; ORGANISM: human
US-10-090-183-2

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
    |||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 12
US-10-165-193A-11
; Sequence 11, Application US/10165193A
; Publication No. US20030207391A1
; GENERAL INFORMATION:
; APPLICANT: HELEN PAPPA
; TITLE OF INVENTION: BINDING PROTEIN
; FILE REFERENCE: 1396-1-00
; CURRENT APPLICATION NUMBER: US/10/165,193A
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: PCT/GB00/04693
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: GB9928950.6
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-193A-11

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
    |||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 13
US-10-394-322A-66
; Sequence 66, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-66

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
    |||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
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RESULT 14
US-10-440-464-129
; Sequence 129, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-129

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
    |||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 15
US-10-783-528-61
; Sequence 61, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-783-528-61

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
    |||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 16
US-10-872-198-115
```

; Sequence 115, Application US/10872198
; Publication No. US20050002897A1

GENERAL INFORMATION:

APPLICANT: Ulrich HAUPTS

APPLICANT: Andre KOLTERMANN

APPLICANT: Andreas SCHEIDIG

APPLICANT: Christian VOETSMEIER

APPLICANT: Ulrich Kettling

; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

; FILE REFERENCE: 04156.000204

; CURRENT APPLICATION NUMBER: US/10/872,198

; CURRENT FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 60/543,518

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/524,960

; PRIOR FILING DATE: 2003-11-25

; PRIOR APPLICATION NUMBER: EP 04003058

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: EP 03025871

; PRIOR FILING DATE: 2003-11-11

; PRIOR APPLICATION NUMBER: EP 03025851

; PRIOR FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: EP 03013819

; PRIOR FILING DATE: 2003-06-18

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 115

; LENGTH: 1356

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-872-198-115

Query Match 100.0%; Score 208; DB 5; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195

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Db 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 18

US-10-741-600-1469

; Sequence 1469, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1469

; LENGTH: 1356

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-600-1469

Query Match 100.0%; Score 208; DB 5; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195

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; Sequence 7, Application US/10763276
; Publication No. US20050004003A1

GENERAL INFORMATION:

APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

; TITLE OF INVENTION: Substance which inhibits binding of information

; TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/Flk-1

; FILE REFERENCE: 249-199

; CURRENT APPLICATION NUMBER: US/10/763,276

; CURRENT FILING DATE: 2004-01-26

; PRIOR APPLICATION NUMBER: US/09/969,037B

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: JP 2000-303694

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: US 60/263,512

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1356

; TYPE: PRT

; ORGANISM: Human

US-10-763-276-7

Query Match 100.0%; Score 208; DB 5; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195

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; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 60/498,407
; PRIOR FILING DATE: 2003-08-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-806-10

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 21
US-10-824-982-2
; Sequence 2, Application US/10824982
; Publication No. US20050197492A1
; GENERAL INFORMATION:
; APPLICANT: Inventors: Michele A. McTigue, Steven L. Bender, Allen Borchardt, Robert
; APPLICANT: S.
; APPLICANT: Kania, Chris Pinko, John A. Wickersham
; TITLE OF INVENTION: Crystal Structure of VEGFRK2: Ligand Complexes and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: PC19173A
; CURRENT APPLICATION NUMBER: US/10/824,982
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-824-982-2

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 22
US-11-021-951-115
; Sequence 115, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTIS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMIEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-115

Query Match      100.0%; Score 208; DB 6; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 23
US-10-090-183-6
; Sequence 6, Application US/10090183
; Publication No. US20030185802A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ralph A. Reisfeld
; APPLICANT: Andrew G. Niethammer
; APPLICANT: Rong Xiang
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-829.0
; CURRENT APPLICATION NUMBER: US/10/090,183
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1345
; TYPE: PRT
; ORGANISM: mouse
US-10-090-183-6

Query Match      98.6%; Score 205; DB 4; Length 1345;
Best Local Similarity 97.6%; Pred. No. 5.7e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 24
US-09-919-408-6
; Sequence 6, Application US/09919408
; Patent No. US20020072077A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/919,408
  FILING DATE: 31-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/977,451
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 07/906,397
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: US PCT/US92/05401
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: TW 81102961
  FILING DATE: 15-APR-1992
  APPLICATION NUMBER: US PCT/US92/02750
  FILING DATE: 02-APR-1992
  APPLICATION NUMBER: US 07/813,593
  FILING DATE: 24-DEC-1991
  APPLICATION NUMBER: US 07/793,065
  FILING DATE: 15-NOV-1991
  APPLICATION NUMBER: US 07/728,913
  FILING DATE: 28-JUN-1991
  APPLICATION NUMBER: US 07/679,666
  FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Felt, Irving N.
  REGISTRATION NUMBER: 28,601
  REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 212-645-1405
  TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1367 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-919-408-6

Query Match      98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
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Db      1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 25
US-09-766-678-2
; Sequence 2, Application US/09766678
; Patent No. US20020081650A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
;           Rieau, Werner
;           Millauer, Birgit
;           Gazit, Aviv
;           Levitzki, Alex
; TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
;                   Endothelial Growth Factor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/766,678
  FILING DATE: 25-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/193,829
  FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Coruzzi, Laura A.
  REGISTRATION NUMBER: 30,742
  REFERENCE/DOCKET NUMBER: 7683-060
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212)790-9090
  TELEFAX: (212)869-9741
  TELEX: 66141 PENNIE
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1367 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-766-678-2

Query Match      98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
      |||||
Db      1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 26
US-09-872-136-6
; Sequence 6, Application US/09872136
; Patent No. US20020119545A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
;                   RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/872,136
  FILING DATE: 01-Jun-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/208,786
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US/09/021,324
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US/07/977,451
  FILING DATE: 1992-11-19
  APPLICATION NUMBER: US 07/906,397
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: US PCT/US92/05401
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: TW 81102961
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;
; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-872-136-6

Query Match          98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB      1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

Search completed: December 9, 2005, 11:25:46
Job time : 64 secs
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2	101	48.6	1338	7	US-11-109-156-23	Sequence 23, Appl
3	55	26.4	1663	6	US-10-982-545-6	Sequence 6, Appl
4	50.5	24.3	383	6	US-10-467-657-3226	Sequence 3226, Ap
5	48.5	23.3	170	7	US-11-069-643-12	Sequence 12, Appl
6	48	23.1	478	6	US-10-467-657-3994	Sequence 3994, Ap
7	48	23.1	581	6	US-10-793-626-28	Sequence 28, Appl
8	48	23.1	752	6	US-10-793-626-1036	Sequence 1036, Ap
9	48	23.1	1304	6	US-10-821-234-1648	Sequence 1648, Ap
10	47	22.6	530	6	US-10-878-556A-71	Sequence 71, Appl
11	47	22.6	530	6	US-10-878-556A-148	Sequence 148, App
12	46	22.1	184	6	US-10-131-828A-76	Sequence 76, Appl
13	46	22.1	215	6	US-10-467-657-2286	Sequence 2286, Ap
14	46	22.1	358	6	US-10-467-657-6970	Sequence 6970, Ap
15	46	22.1	434	6	US-10-467-657-6894	Sequence 6894, Ap
16	46	22.1	564	6	US-10-485-517-298	Sequence 298, App
17	45	21.6	136	6	US-10-793-626-1970	Sequence 1970, Ap
18	45	21.6	139	6	US-10-793-626-1644	Sequence 1644, Ap
19	45	21.6	165	6	US-10-793-626-844	Sequence 844, App
20	45	21.6	948	6	US-10-485-517-131	Sequence 131, App
21	45	21.6	1071	6	US-10-467-657-1654	Sequence 1654, Ap
22	45	21.6	4374	7	US-11-128-572-2	Sequence 2, Appl
23	44.5	21.4	205	6	US-10-793-626-2156	Sequence 2156, Ap
24	44.5	21.4	215	6	US-10-793-626-1102	Sequence 1102, Ap
25	44.5	21.4	372	6	US-10-793-626-2840	Sequence 2840, Ap

RESULT 7
US-10-793-626-28
; Sequence 28, Application US/10793626
; Publication No. US20050255478A1

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RESULT 9
US-10-821-234-1648
; Sequence 1648, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07

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;; PRIOR APPLICATION NUMBER: US 60/462,047
;; PRIOR FILING DATE: 2003-04-07
;; NUMBER OF SEQ ID NOS: 1704
;; SOFTWARE: pt seq_genes Version 1.0
;; SEQ ID NO 1648
;; LENGTH: 1304
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-821-234-1648

Query Match 23.1%; Score 48; DB 6; Length 1304;
Best Local Similarity 36.8%; Pred. No. 71;
Matches 14; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

Qy 1 SELVEHLGNLQAQAQDGKDYI--VLPISETLSMEED 36
Db 1152 SFLEFYIGEM-----GKDYIYAVTPLLBDALMDRD 1181

RESULT 10
US-10-878-556A-71
;; Sequence 71, Application US/10878556A
;; Publication No. US20050266399A1
;; GENERAL INFORMATION:
;; APPLICANT: Hoffmann La-Roche Inc.
;; TITLE OF INVENTION: HCV regulated protein expression
;; FILE REFERENCE: 21762
;; CURRENT APPLICATION NUMBER: US/10/878,556A
;; CURRENT FILING DATE: 2004-06-28
;; NUMBER OF SEQ ID NOS: 199
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 71
;; LENGTH: 530
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: sw_hum/kpy2_human
;; DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-71

Query Match 22.6%; Score 47; DB 6; Length 530;
Best Local Similarity 27.3%; Pred. No. 33;
Matches 9; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 10 LLOANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 179 LISLQVKQKGADFLVTEVNGGSLGSKGVNLP 211

RESULT 11
US-10-878-556A-148
;; Sequence 148, Application US/10878556A
;; Publication No. US20050266399A1
;; GENERAL INFORMATION:
;; APPLICANT: Hoffmann La-Roche Inc.
;; TITLE OF INVENTION: HCV regulated protein expression
;; FILE REFERENCE: 21762
;; CURRENT APPLICATION NUMBER: US/10/878,556A
;; CURRENT FILING DATE: 2004-06-28
;; NUMBER OF SEQ ID NOS: 199
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 148
;; LENGTH: 530
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: sw_hum/kpy1_human
;; DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-148

Query Match 22.6%; Score 47; DB 6; Length 530;
Best Local Similarity 27.3%; Pred. No. 33;
Matches 9; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 10 LLOANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 179 LISLQVKQKGADFLVTEVNGGSLGSKGVNLP 211

RESULT 12
US-10-131-826A-76
;; Sequence 76, Application US/10131826A
;; Publication No. US20050245730A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: Berorge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3330R1C128
;; CURRENT APPLICATION NUMBER: US/10/131,826A
;; CURRENT FILING DATE: 2002-04-24
;; PRIOR APPLICATION NUMBER: 60/049911
;; PRIOR FILING DATE: 1997-06-18
;; PRIOR APPLICATION NUMBER: 60/056974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059115
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059117
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 76
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-131-826A-76

Query Match 22.1%; Score 46; DB 6; Length 184;
Best Local Similarity 31.7%; Pred. No. 12;
Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 4 VEHLGNL-LQANAQQDGKDYI-VLPISETLSMEEDSGLSLP 42
Db 96 LQHLKAIDLGRNQDFFPEQLTALPALETINLENEIVDVP 136

RESULT 13
US-10-467-657-2286
;; Sequence 2286, Application US/10467657

; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2286
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2286

Query Match 22.1%; Score 46; DB 6; Length 215;
Best Local Similarity 28.2%; Pred. No. 15;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
QY 4 VEHGLNLLQANAQQDGKDYIVLPISSETLSMEEDSGLSLP 42
Db 171 VOGIGFIQSIQSGSPGIMGLPVYETVSMQLDLYRPP 209

RESULT 14
US-10-467-657-6970
; Sequence 6970, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6970
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6970

Query Match 22.1%; Score 46; DB 6; Length 358;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 13; Indels 2; Gaps 1;
QY 5 EHLGNLLQANAQQDGKDYIVLPISSETLSMEED 36
Db 132 EHLKNLLEKNVGKFDRTFIV--TESVFSMDGD 161

RESULT 15
US-10-467-657-6894
; Sequence 6894, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6894
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6894
Query Match 22.1%; Score 46; DB 6; Length 434;
Best Local Similarity 26.4%; Pred. No. 35;
Matches 14; Conservative 11; Mismatches 12; Indels 16; Gaps 2;
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Db 56 HIGLLHRTGTEKLAETKTLYLQALPYMDRLDYVSMYNEQAYCLAVEKLAGIDVP 108
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OM protein - protein search, using sw model

Run on: December 9, 2005, 11:21:24 ; Search time 186 Seconds
(without alignments)
99.215 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195
Perfect score: 208
Sequence: 1 SELVEHLGNLQNAQQDGK.....IVLPISETLSMEEDSGLSLP 42

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	429	9 ADY85472	Ady85472 Catalytic
2	208	100.0	1306	8 ADQ39807	Adq39807 Human myo
3	208	100.0	1354	9 ADZ00446	Adz00446 VEGFR-2.
4	208	100.0	1355	2 AAW80997	Aaw80997 Human rec
5	208	100.0	1356	2 AAR26999	Aar26999 Novel typ
6	208	100.0	1356	2 AAW59275	Aaw59275 Human KDR
7	208	100.0	1356	2 AAB62475	Aab62475 Human VEG
8	208	100.0	1356	4 AAY97783	Aay97783 Human KDR
9	208	100.0	1356	4 AAU97576	Aau97576 Human Flk
10	208	100.0	1356	5 AAU79427	Aau79427 Human Kin
11	208	100.0	1356	5 AAU79429	Aau79429 Human Kin
12	208	100.0	1356	5 AAU79426	Aau79426 Human Kin
13	208	100.0	1356	6 ABR40196	Abr40196 Human vas
14	208	100.0	1356	7 ADD08954	Add08954 Human VEG
15	208	100.0	1356	7 ABM79007	Abm79007 Human VEG
16	208	100.0	1356	7 ADF45097	Adf45097 Human kin
17	208	100.0	1356	7 ABU64302	Abu64302 Human KDR
18	208	100.0	1356	8 ADH17130	Adh17130 Human vas
19	208	100.0	1356	8 ADG70543	Adg70543 Human KDR
20	208	100.0	1356	8 ADQ39806	Adq39806 Human myo
21	208	100.0	1356	8 ADQ39808	Adq39808 Human myo
22	208	100.0	1356	8 ADRA6648	Adra6648 Cancer-as
23	208	100.0	1356	8 ADT92353	Adt92353 Human vas
24	208	100.0	1356	9 ADV90285	Adv90285 Protease-

25	208	100.0	1356	9 ADY59385	Ady59385 Human VEG
26	208	100.0	1356	9 ADZ26561	Adz26561 Human VEG
27	205	98.6	558	8 ADR32352	Adr32352 Rat recep
28	205	98.6	820	8 ADR32354	Adr32354 GST-rat K
29	205	98.6	1343	8 ADR32351	Adr32351 Rat recep
30	205	98.6	1343	8 ADR32338	Adr32338 Rat Optim
31	205	98.6	1345	7 ABM79009	Abm79009 Murine Fl
32	205	98.6	1367	2 AAR28041	Aar28041 flk-1. 3/
33	205	98.6	1367	2 AAR31377	Aar31377 Human flk
34	205	98.6	1367	2 AAR37504	Aar37504 Murine fl
35	205	98.6	1367	2 AAR44996	Aar44996 Murine fl
36	205	98.6	1367	2 AAR54046	Aar54046 Sequence
37	205	98.6	1367	2 AAR67537	Aar67537 Mouse flk
38	205	98.6	1367	2 AAR67817	Aar67817 Flk1 rece
39	205	98.6	1367	2 AAR97420	Aar97420 Murine fo
40	205	98.6	1367	2 AAW19875	Aaw19875 Murine fl
41	205	98.6	1367	2 ADP90725	Adp90725 Mouse foe
42	205	98.6	1367	2 AAY08618	Aay08618 Murine fl
43	205	98.6	1367	5 ABG70917	Abg70917 Mouse rec
44	205	98.6	1367	5 AAE25820	Aae25820 Murine re
45	205	98.6	1367	6 ABR40197	Abr40197 Murine va

ALIGNMENTS

RESULT 1
ADY85472
ID ADY85472 standard; protein; 429 AA.
XX
AC ADY85472;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein VEGFR.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
(PLEX-) PLEXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands

CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII) preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group), and developing a ligand for a kinase
CC comprising conserved residues matching at least one of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.

XX SQ Sequence 429 AA;

Query Match 100.0%; Score 208; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 2.2e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 371 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 412

RESULT 2

ADQ39807

ID ADQ39807 standard; protein; 1306 AA.

XX AC ADQ39807;

XX AC 18-NOV-2004 (first entry)

XX DT Human myocardial infarction-associated gene derived protein, SEQ ID 1470.

XX DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX KW cardiant; gene therapy; human.

XX KW Homo sapiens.

XX OS WO2004058052-A2.

XX PN 15-JUL-2004.

XX PD 22-DEC-2003; 2003WO-US040978.

XX PF

XX PR 20-DEC-2002; 2002US-0434778P.

XX PR 10-MAR-2003; 2003US-0453135P.

XX PR 30-APR-2003; 2003US-0466412P.

XX PR 23-SEP-2003; 2003US-0504955P.

XX PA (APPL-) APPLERA CORP.

XX XX Cargill M, Devlin JJ, Iakoubova O;

XX P1 WPI; 2004-533949/51.

XX XX N-PSDB; ADQ38979.

XX DR Identifying an individual who has an altered risk for developing

XX PT myocardial infarction by detecting a single nucleotide polymorphism in

XX PT the individual's nucleic acids.

XX PS Claim 10; SEQ ID NO 1470; 145pp; English.

XX CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1306 AA;

Query Match 100.0%; Score 208; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 9.5e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1104 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1145

RESULT 3

ADZ00446

ID ADZ00446 standard; protein; 1354 AA.

XX AC ADZ00446;

XX DT 16-JUN-2005 (first entry)

XX DE VEGFR-2.

XX XX VEGF-C agonist; VEGF-D agonist; Nootropic; Neuroprotective;

XX KW Antiparkinsonian; Anticonvulsant; CNS-Gen.; Antiinflammatory; Anti-HIV;

XX KW Virucide; Vasotropic; vascular endothelial growth factor C; VEGF-C;

XX KW vascular endothelial growth factor D; VEGF-D; recruitment; proliferation;

XX KW differentiation; migration; survival; neural cell; precursor; VEGFR-3;

KW neotropin-2; VEGF-C deltaC156; heparin-binding VEGF-C;
KW neurotherapeutic; interferon gamma; nerve growth factor;
KW epidermal growth factor; EGF; basic fibroblast growth factor; bFGF;
KW neurogenin; brain derived neurotrophic factor; BDNF; thyroid hormone;
KW bone morphogenic protein; BMP; leukemia inhibitory factor; LIF;
KW sonic hedgehog; glial cell line-derived neurotrophic factor; GDNF;
KW vascular endothelial growth factor; VEGF; interleukin; interferon;
KW stem cell factor; SCF; activin; inhibin; chemokine; retinoic acid;
KW ciliary neurotrophic factor; CNTF; tacrine; Cognex; donepezil; Aricept;
KW rivastigmine; Exelon; galantamine; Reminyl; cholinesterase inhibitor;
KW anti-inflammatory; anti-cholinergic; dopamine agonist;
KW catechol-O-methyl-transferase; COMT; amantadine; Symmetrel; Sinemet;
KW Selegiline; carbidopa; ropinirole; Requip; coenzyme Q10; Pramipexole;
KW Mirapex; levodopa; L-dopa; Alzheimers disease; Parkinsons disease;
KW Huntingtons disease; motor neuron disease;
KW Amyotrophic lateral Sclerosis; ALS; dementia; cerebral palsy;
KW demyelination; multiple sclerosis; phenylketonuria;
KW periventricular leukomalacia; PVL; HIV-1 encephalitis; HIVE;
KW Guillian Barre Syndrome; GBS;
KW acute inflammatory demyelinating polyneuropathy; AIDP;
KW acute motor axonal neuropathy; AMAN;
KW acute motor sensory axonal neuropathy; AMSAN; Fisher syndrome;
KW acute pandysautonomia;
KW chronic inflammatory demyelinating polyradiculoneuropathy; CIDP;
KW multifocal acquired demyelinating sensory and motor neuropathy; MADSAM;
KW Lewis-Sumner syndrome;
KW distal acquired demyelinating symmetric neuropathy; DADS; neural trauma;
KW neural injury; stroke; spinal cord injury; post-operative injury;
KW brain ischemia; neuroblastoma; neural tumor.
XX Homo sapiens.
XX
XX WO2005030240-A2.
XX
XX 07-APR-2005.
XX
XX 23-SEP-2004; 2004WO-US031318.
XX
XX 23-SEP-2003; 2003US-00669176.
XX 23-SEP-2003; 2003US-0505607P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Alitalo K, Karkainen M, Haiko P, Sainio K, Wartiovaara K;
XX Thomas JL, Eichmann A;
XX
XX WPI: 2005-273287/28.
XX N-PSDB; ADZ00445.
XX GENBANK; L04947.
XX
XX Use of a vascular endothelial growth factor-C or -D product in
XX medicaments for promoting growth and differentiation of neural stem cells
XX for neurodegenerative disorders such as Alzheimer's and Parkinson's
XX disease.
XX
XX Disclosure; SEQ ID NO 28; 263pp; English.
XX
XX This sequence represents VEGFR-2. The method of the invention uses a
XX vascular endothelial growth factor-C (VEGF-C) product or a vascular
XX endothelial growth factor D (VEGF-D) product in the manufacture of a
XX medicament to promote recruitment, proliferation, differentiation,
XX migration or survival of neural cells or neural precursor cells. The
XX method of the invention comprises identifying a mammalian subject in need
XX of treatment to promote recruitment, proliferation, differentiation,
XX migration, or survival of neural cells or neural precursor cells, and
XX administering to the subject a composition comprising a VEGF-C or VEGF-D
XX product. The product is a VEGF-C product comprising a purified mammalian
XX prepro-VEGF-C polypeptide or its fragment that binds VEGFR-3 or
XX neotropin-2, a VEGF-C deltaC156 polypeptide, or a chimeric heparin-
XX binding VEGF-C polypeptide. The method also comprises administering to
XX the mammalian subject a neurotherapeutic agent, and including in the

CC medicament a neurotherapeutic agent. The neurotherapeutic agent comprises
CC a neural growth factor and/or a polynucleotide encoding a neural growth
CC factor selected from interferon gamma, nerve growth factor, epidermal
CC growth factor (EGF), basic fibroblast growth factor (bFGF), neurogenin,
CC brain derived neurotrophic factor (BDNF), thyroid hormone, bone
CC morphogenic proteins (BMPs), leukemia inhibitory factor (LIF), sonic
CC hedgehog, glial cell line-derived neurotrophic factor (GDNF), vascular
CC endothelial growth factor (VEGF), interleukins, interferons, stem cell
CC factor (SCF), activins, inhibins, chemokines, retinoic acid and ciliary
CC neurotrophic factor (CNTF). The neurotherapeutic agent is also tacrine
CC (Cognex), donepezil (Aricept), rivastigmine (Exelon), galantamine
CC (Reminyl), cholinesterase inhibitors or anti-inflammatory drugs, and/or
CC is anti-cholinergics, dopamine agonists, catechol-O-methyl-transferases
CC (COMT), amantadine (Symmetrel), Sinemet (RPM), Selegiline, carbidopa,
CC ropinirole (Requip), coenzyme Q10, Pramipexole (Mirapex) and levodopa (L-
CC dopa). The medicament of the invention is for the treatment of a disease
CC or condition characterized by aberrant growth of neuronal cells, neuronal
CC scarring, or neural degeneration, or for treatment of neural degeneration
CC caused by a neurodegenerative disorder selected from the group consisting
CC of is Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC motor neuron disease, Amyotrophic Lateral Sclerosis (ALS), dementia and
CC cerebral palsy, and for treatment of a disease or condition with aberrant
CC growth of oligodendrocyte or oligodendrocyte precursor cells, where the
CC condition has demyelination in the nervous system. The medicament is also
CC for the treatment of multiple sclerosis, phenylketonuria, periventricular
CC leukomalacia (PVL), HIV-1 encephalitis (HIVE), Guillian Barre Syndrome
CC (GBS), acute inflammatory demyelinating polyneuropathy (AIDP), acute
CC motor axonal neuropathy (AMAN), acute motor sensory axonal neuropathy
CC (AMSAN), Fisher syndrome, acute pandysautonomia, and Krabbe's disease.
CC The medicament can also be used for the treatment of chronic inflammatory
CC demyelinating polyradiculoneuropathy (CIDP), such as multifocal acquired
CC demyelinating sensory and motor neuropathy (MADSAM, also know as Lewis-
CC Sumner syndrome) and distal acquired demyelinating symmetric neuropathy
CC (DADS), and for the treatment of neural trauma or neural injury, where
CC the neural trauma is a stroke-related injury, spinal cord injury, post-
CC operative injury or brain ischemia. The VEGF-C inhibitor is useful in the
CC manufacture of a medicament for the treatment of a neuroblastoma or
CC neural tumor. The methods and compositions of the present invention are
CC also useful for cellular and molecular biology and medicine, in
CC particular for the vascularization and angiogenesis and the interactions
CC of the vascular system with the nervous system.
XX
XX Sequence 1354 AA;
XX
XX Query Match 100.0%; Score 208; DB 9; Length 1354;
XX Best Local Similarity 100.0%; Pred. No. 1e-20;
XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SELVEHLGNLQANAQQDGKDYIVLPISFTLSMEEDSGLSLP 42
XX |||||
XX Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISFTLSMEEDSGLSLP 1193
XX
XX RESULT 4
XX ID AAW80997
XX AC AAW80997
XX AC AAW80997;
XX
XX DT 12-APR-1999 (first entry)
XX DE Human receptor tyrosine kinase KDR.
XX
XX KW KDR; receptor tyrosine kinase; human; signal transduction; mitogen;
XX KW neangiogenesis; angiogenesis; diabetic retinopathy; breast cancer;
XX KW brain cancer; inflammation; rheumatoid arthritis; psoriasis;
XX KW contact dermatitis; hypersensitivity; antagonist; therapy.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Domain 780..1386
XX FT /note= "intracellular domain, from about amino acid 780-

```

XX 795 to about amino acid 1175-1386"
XX WO9858053-A1.
XX 23-DEC-1998.
XX 17-JUN-1998; 98WO-US012569.
XX 18-JUN-1997; 97US-0050962P.
XX (MERI ) MERCK & CO INC.
XX Kendall RL, Thomas KA, Mao X, Tebben A;
XX WPI; 1999-095333/08.
XX N-PSDB; AAV99829.
XX Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for
XX antagonists useful to treat diseases involving neoangiogenesis e.g.
XX diabetic retinal vascularization, cancers.
XX Claim 2; Fig 2; 69pp; English.
XX This is the amino acid sequence of a novel receptor tyrosine kinase,
XX termed KDR, that is expressed on human endothelial cells. KDR is
XX activated by vascular endothelial growth factor and mediates a mitogenic
XX signal. It is implicated in clinical neoangiogenesis. The amino acid
XX sequence was deduced from an isolated KDR cDNA (see AAV99829). The
XX predicted sequence has differences from the previously published KDR
XX sequence at positions 498 (Ala to Glu), 772 (Thr to Ala), 787 (Gly to
XX Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Thr to Ser), producing
XX a protein predicted by computer modeling to have higher activity and
XX functionality. The invention also relates to recombinant vectors and
XX recombinant hosts which contain a DNA fragment encoding human KDR, a DNA
XX fragment encoding the intracellular portion of KDR with or without a
XX membrane anchor sequence, purified forms of associated human KDR, and
XX human mutant forms of KDR. KDR, fusion proteins or fragments can be used
XX in assays to identify antagonists and agonists of human KDR (Claimed).
XX Antagonists of KDR useful for treating diseases involving neoangiogenesis
XX e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.)
XX and forms of inflammation e.g. rheumatoid arthritis, psoriasis, contact
XX dermatitis and hypersensitivity reactions. The protein is also useful for
XX produce antibodies that can be used to measure human KDR levels and/or
XX activity
XX
XX Sequence 1355 AA;
XX
XX Query Match 100.0%; Score 208; DB 2; Length 1355;
XX Best Local Similarity 100.0%; Pred. No. 1e-20;
XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
XX |||||||||||||||||||||||||||||||||||||||||||
XX Db 1153 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1194
XX
XX RESULT 5
XX AAR26999
XX ID AAR26999 standard; protein; 1356 AA.
XX
XX AC AAR26999;
XX
XX 23-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 20-MAY-1998 (first entry)
XX
XX Novel type III RTK encode by the KDR gene.
XX
XX Receptor tyrosine kinase; vascular endothelial cell growth factors;
XX cancer; tumour; diagnosing; monitoring.
XX
XX Homo sapiens.
XX OS Unidentified.

```

```

XX PH Location/Qualifiers
XX Domain 1. .763
XX /note= "putative extracellular region - contains 21
XX cysteine residues"
XX
XX Modified-site 46
XX /note= "potential N linked glycosylation site"
XX
XX Modified-site 66
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 96
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 143
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 158
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 245
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 318
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 374
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 395
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 511
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 523
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 580
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 613
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 631
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 675
XX /note= "potential N-linked glycosylation site"
XX
XX Modified-site 704
XX /note= "potential N-linked glycosylation site"
XX
XX Domain 764. .788
XX /note= "putative membrane spanning region"
XX
XX Domain 868
XX /note= "ATP binding site"
XX
XX WO9214748-A1.
XX
XX 03-SEP-1992.
XX
XX 20-FEB-1992; 92WO-US001300.
XX
XX 22-FEB-1991; 91US-00657236.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Terman BI, Carrion ME;
XX
XX WPI; 1992-316117/38.
XX N-PSDB; AAQ28272.
XX
XX DNA encoding type III receptor tyrosine kinase - useful for diagnosing
XX the onset of cancer.
XX
XX Claim 3; Fig 7; 101pp; English.
XX
XX This sequence represents a novel type III receptor tyrosine kinase
XX encoded by the KDR gene. It was decoded from the appropriate cDNA, and
XX its predicted amino acid sequence contains several features which
XX demonstrate that the novel gene is a type III RTK. A hydrophathy plot of
XX the predicted amino acid sequence indicates a single membrane spanning
XX region. The putative amino terminal 762 amino acids of the receptor has
XX structural features of extracellular receptor ligand binding domains,
XX including regularly spaced cysteines, and 18 potential N-linked
XX glycosylation sites. The predicted amino acid sequence of the COOH
XX terminal 530 amino acid portion contains an ATP binding site at lysine
XX 868, 22 amino acids downstream from the consensus ATP recognition

```

CC sequence. Within the kinase domain there is a 55-60% identical match in
CC amino acid sequence to 3 other type III receptor tyrosine kinases: ckit
CC proto-oncogene, CSF-1 and PDGF. The predicted kinase domain contains a
CC kinase insert domain of approximately 71 amino acids, sharing little
CC homology with other type III RTKs. (Updated on 25-MAR-2003 to correct PN
CC field.)

CC Revised record issued on 23-SEP-2004 : Correction to Feature Table Key

XX Sequence 1356 AA;

SQ Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 6

AAW59275
ID AAW59275 standard; protein; 1356 AA.

XX AC

AAW59275;

XX 27-AUG-1998 (first entry)

DT Human KDR protein.

DE Kinase insert domain containing receptor; KDR; screening; inhibitor;
KW vascular endothelial growth factor; VEGF; angiogenesis; treatment;
KW cancer.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Modified-site 45
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 66
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 96
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 143
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 158
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 245
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 318
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 374
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 395
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 511
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 580
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 613
FT /label= N-glycosylated
FT /note= "putative"

FT Modified-site 631
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 675
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 704
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 721
FT /label= N-glycosylated
FT /note= "putative"
FT Region 765..789
FT /note= "putative membrane spanning region"
XX US5766860-A.
XX 16-JUN-1998.
XX 25-FEB-1997; 97US-00810116.
XX 23-NOV-1992; 92US-00930548.
XX (AMCY) AMERICAN CYANAMID CO.
XX Terman BI, Carrion ME;
XX WPI, 1998-361682/31.
XX N-PSDB; AAV34763.
XX Screening assay for vascular endothelial cell growth factor antagonists -
FT using recombinant cells expressing receptor protein.
XX Claim 1; Fig 7A-M; 51pp; English.
XX This sequence represents a novel human growth factor receptor, kinase
CC insert domain containing receptor or KDR. This receptor is capable of
CC binding to the vascular endothelial cell growth factor, VEGF and is used
CC in a screening assay which identifies compounds that inhibit VEGF action
CC on KDR. Such compounds which inhibit binding of VEGF to the KDR may
CC inhibit angiogenesis and thus be useful for treating cancer
XX Sequence 1356 AA;
Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 7
AAB62475
ID AAB62475 standard; protein; 1356 AA.
XX AC
XX AAB62475;
XX 09-JUL-2001 (first entry)
XX Human VEGFR-2 receptor protein.
XX Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2;
KW neuropilin-1; NP-1; co-receptor; human; angiogenic.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Domain 1..760
FT /note= "extracellular domain"
FT Domain 124..320
FT /note= "Ig domain"

```
XX WO200131346-A2.
XX
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029579.
XX
XX PR 28-OCT-1999; 99US-0162367P.
XX
XX PA (PROC ) PROCTER & GAMBLE CO.
XX
XX PI Rosenbaum JS, Whitaker GB, Limberg BJ;
XX
XX DR WPI; 2001-308686/32.
XX
XX DR N-PSDB; AAF83308.
XX
XX PT Determining compounds which bind to a complex comprising vascular
XX PT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior
XX PT pro- and anti-angiogenic agents.
XX
XX PS Claim 7; Page 32-39; 82pp; English.
XX
XX CC The invention relates to determining whether a compound is capable of
XX CC binding to a receptor protein complex comprising a vascular endothelial
XX CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
XX CC (NP-1) receptor protein. One method comprises introducing a sample
XX CC comprising the compound to the receptor protein and allowing the compound
XX CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the
XX CC presence of the NP-1 co-receptor. The methods of the invention can be
XX CC used for identifying novel pro- and anti-angiogenic compounds. The
XX CC present sequence represents the human VEGFR-2 receptor protein
XX
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 9
AA97576
ID AAY97576 standard; protein; 1356 AA.
XX
XX AC AAY97576;
XX
XX DT 05-APR-2001 (first entry)
XX
XX DE Human Flk-1 transmembrane and extracellular domains.
XX
XX KW Human; angiogenic protein; wound healing; vascular tissue repair;
XX KW peripheral arterial disease; critical limb ischaemia; coronary disease;
XX KW angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
XX KW rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
XX KW infectious disease; neurodegeneration; Flk-1.
XX
XX OS Homo sapiens.
XX
XX PN WO200075163-A1.
XX
XX PD 14-DEC-2000.
XX
XX PF 01-JUN-2000; 2000WO-US014925.
XX
XX PR 03-JUN-1999; 99US-0137796P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM, Hu J, Cao L;
XX
XX DR WPI; 2001-071057/08.
XX
XX PT New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
XX PT healing of wounds and treating peripheral arterial disease, critical limb
XX PT ischemia or coronary disease.
XX
XX PS Example 48; Page 236-240; 244pp; English.
XX
XX CC This sequence is a human Flk-1 fragment, and was used in the isolation of
XX CC an angiogenic protein of the invention. The angiogenic proteins and the
XX CC DNA sequences encoding them, are used to prevent, treat or ameliorate
XX CC disease and to detect diseases, or susceptibility, by detecting mutations
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XX WO200131346-A2.
XX
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029579.
XX
XX PR 28-OCT-1999; 99US-0162367P.
XX
XX PA (PROC ) PROCTER & GAMBLE CO.
XX
XX PI Rosenbaum JS, Whitaker GB, Limberg BJ;
XX
XX DR WPI; 2001-308686/32.
XX
XX DR N-PSDB; AAF83308.
XX
XX PT Determining compounds which bind to a complex comprising vascular
XX PT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior
XX PT pro- and anti-angiogenic agents.
XX
XX PS Claim 7; Page 32-39; 82pp; English.
XX
XX CC The invention relates to determining whether a compound is capable of
XX CC binding to a receptor protein complex comprising a vascular endothelial
XX CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
XX CC (NP-1) receptor protein. One method comprises introducing a sample
XX CC comprising the compound to the receptor protein and allowing the compound
XX CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the
XX CC presence of the NP-1 co-receptor. The methods of the invention can be
XX CC used for identifying novel pro- and anti-angiogenic compounds. The
XX CC present sequence represents the human VEGFR-2 receptor protein
XX
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 8
AA97783
ID AAY97783 standard; protein; 1356 AA.
XX
XX AC AAY97783;
XX
XX DT 22-AUG-2001 (first entry)
XX
XX DE Human KDR/Flk-1 protein.
XX
XX KW Immunoglobulin-like domain; Ig-like domain; retinal neovascularisation;
XX KW vascular endothelial growth factor receptor; VEGF receptor; inflammation;
XX KW psoriasis; rheumatoid arthritis; haemangioma; leiomyoma; angiofibroma;
XX KW diabetic retinopathy; endometriosis; macular degeneration; cancer;
XX KW dimerisation inhibitor; therapy; KDR/Flk-1; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200142284-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 07-DEC-2000; 2000WO-GB004693.
XX
XX PR 07-DEC-1999; 99GB-00028950.
XX
XX PA (METR-) METRIS THERAPEUTICS LTD.
XX
XX PI Pappa H;
XX
```

or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also used for stimulating (lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating regeneration of the nervous system etc

XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 4; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 10

AAU79427
 ID AAU79427 standard; protein; 1356 AA.

XX AC AAU79427;

XX DT 02-JUL-2002 (first entry)

XX DE Human Kinase insert domain-containing receptor mutant Y801P.

XX KW Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
 KW fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic; mutein;
 KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
 KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 801 /note= "Wild-type Tyr substituted by Phe"

XX PN WO200229090-A1.

XX PD 11-APR-2002.

XX PF 02-OCT-2001; 2001WO-JP008684.

XX PR 03-OCT-2000; 2000JP-00303694.

XX XX (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (SHIB/) SHIBUYA M.

XX XX Shibuya M, Takahashi T, Furuya A, Shitara K;

XX XX WPI; 2002-352237/38.

XX XX Screening substances inhibiting the binding of signal-transducing
 PT molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
 PT cell proliferation inhibitors and angiogenesis inhibitors for treatment
 PT of e.g. tumor.

XX Example 8; Page; 81pp; Japanese.

PS The invention relates to inhibiting the signal transduction of KDR/Flk-1
 CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
 CC using a substance inhibiting the binding of a signal-transducing molecule
 CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
 CC included are methods of detecting/inhibiting/screening for cell
 CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
 CC phosphorylation at tyrosine at the 1175-position using the binding
 CC inhibitors, compounds obtained by the screening methods, drugs containing
 CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-1
 CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
 CC monoclonal antibody or its fragment, a recombinant vector containing the
 CC DNA and a transformant obtained by transferring the recombinant vector
 CC into a host cell. The method is useful for screening substances
 CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
 CC phosphorylated at tyrosine at 1175-position, as cell proliferation
 CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
 CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
 CC detecting angiogenesis is also provided. The present sequence is the
 CC Human KDR/FLK-1 mutant where Tyr at 801 is replaced by Phe. Note: The
 CC present sequence is not shown in the specification but was created by the
 CC indexer using the KDR/FLK-1 sequence appearing as AAU74926 and the
 CC information in example 8

XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 5; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||

Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 11

AAU79429

ID AAU79429 standard; protein; 1356 AA.

XX AC AAU79429;

XX DT 02-JUL-2002 (first entry)

XX DE Human Kinase insert domain-containing receptor mutant Y1214F.

XX KW Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
 KW fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic; mutein;
 KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
 KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1214 /note= "Wild-type Tyr substituted by Phe"

XX PN WO200229090-A1.

XX PD 11-APR-2002.

XX XX 02-OCT-2001; 2001WO-JP008684.

XX PR 03-OCT-2000; 2000JP-00303694.

XX XX (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (SHIB/) SHIBUYA M.

XX XX Shibuya M, Takahashi T, Furuya A, Shitara K;

XX XX WPI; 2002-352237/38.

```

XX Screening substances inhibiting the binding of signal-transducing
PT molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT of e.g. tumor.
XX
PS Example 8; Page; 81pp; Japanese.
XX
CC The invention relates to inhibiting the signal transduction of KDR/Flk-1
CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
CC using a substance inhibiting the binding of a signal-transducing molecule
CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
CC included are methods of detecting/inhibiting/screening for cell
CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
CC phosphorylation at tyrosine at the 1175-position using the binding
CC inhibitors, compounds obtained by the screening methods, drugs containing
CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk
CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
CC monoclonal antibody or its fragment, a recombinant vector containing the
CC DNA and a transformant obtained by transferring the recombinant vector
CC into a host cell. The method is useful for screening substances
CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
CC phosphorylated at tyrosine at 1175-position, as cell proliferation
CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
CC detecting angiogenesis is also provided. The present sequence is the
CC present sequence is not shown in the specification but was created by the
CC indexer using the KDR/FLK-1 sequence appearing as AAU74926 and the
CC information in example 8
XX
SQ Sequence 1356 AA;

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||
1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 12
AAU79426
ID AAU79426 standard; protein; 1356 AA.
XX
AC AAU79426;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human Kinase insert domain-containing receptor.
XX
KW Human; KDR; kinase insert domain-containing; receptor; FLK-1;
KW fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic;
KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200229090-A1.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-JP008694.
XX
PR 03-OCT-2000; 2000JP-00303694.
XX
PA (KYOWA) KYOWA HAKKO KOGYO KK.
PA (SHIBUYA) SHIBUYA M.
XX
PI Shibuya M, Takahashi T, Furuya A, Shitara K;
XX WPI; 2002-352237/38.
XX
DR

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||
1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 13
ABR40196
ID ABR40196 standard; protein; 1356 AA.
XX
AC ABR40196;
XX
DT 01-AUG-2003 (first entry)
XX
DE Human vascular endothelial growth factor receptor-2.
XX
KW Human; vascular endothelial growth factor receptor-2; cytostatic;
KW angiogenic; antiangiogenic; antiarthritic; antirheumatic; antisense;
KW VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis;
KW angiogenesis.
XX
OS Homo sapiens.
XX
PN WO2003029266-A1.
XX
PD 10-APR-2003.
XX
PF 26-SEP-2002; 2002WO-US030734.
XX
PR 28-SEP-2001; 2001US-00967655.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Watt AT;
XX WPI; 2003-371980/35.
XX
DR N-ESDB; ACC71713.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding vascular endothelial growth factor receptor-2

```

PT (VEGFR-2), useful for treating a disease/condition associated with VEGFR-2, e.g. cancer.

PS Example 13; Page 90-97; 127pp; English.

XX The present invention relates to novel antisense oligonucleotides (ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and CC which inhibit the expression of VEGFR-2. The oligonucleotides are useful CC in compositions for treating a disease or condition associated with VEGFR CC -2, such as hyperproliferative disorder, e.g. cancer, a disease or CC condition involving angiogenesis, or rheumatoid arthritis. The present CC sequence is human VEGFR-2

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 6; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 14

ID ADD08954 standard; protein; 1356 AA.

AC ADD08954;

XX 01-JAN-2004 (first entry)

DE Human VEGFR-2 protein SEQ ID NO:30.

XX screening; modulator; binding; neuropilin growth factor receptor;
KW vascular endothelial growth factor C;
KW vascular endothelial growth factor receptor 3; VEGF-C; VEGFR-3;
KW neuropilin; cytosolic; nontropic; neuroprotective; vulnary;
KW vasotrophic; cardiant; angiogenic process; nervous system growth;
KW nervous system function; cancer; ischaemia; cerebral infarction;
KW cerebral bleeding; Alzheimer's disease; myocardial infarction; human.

XX Homo sapiens.

XX WO2003029814-A2.

XX 10-APR-2003.

XX 01-OCT-2002; 2002WO-EP0111069.

XX 01-OCT-2001; 2001US-0326326P.

XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.

XX Alitalo K, Karkkainen M, Karila K;

XX WPI; 2003-381660/36.

XX N-PSDB; ADD08953.

XX Screening for modulators of neuropilin and vascular endothelial growth
PT factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction
PT of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a
PT modulator compound.

XX Disclosure; SEQ ID NO 30; 181pp; English.

XX The present invention describes a method of screening for modulators of
CC binding between a neuropilin growth factor receptor and a vascular
CC endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising
CC comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the
CC presence and in the absence of a putative modulator compound. Also

CC described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-3 or neuropilin biological activity; (2) modulating growth, migration or CC proliferation of cells in a mammalian organism; (3) a bispecific antibody CC which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3 CC polypeptide; (4) modulating neuronal growth or neuronal scarring in a CC mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF CC -C that binds to a neuropilin receptor. The modulators have cytostatic, CC activities. The method is useful in modulating angiogenic processes and CC nervous system growth and function, such as in the treatment of cancer, CC wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or CC myocardial infarction. The polypeptide comprising a fragment of a VEGF-C CC that binds to a neuropilin receptor, is useful for manufacturing a CC medicament for the treatment of diseases characterised by aberrant CC growth, migration or proliferation of cells that express a neuropilin CC receptor. The present sequence represents human VEGFR-2, which is used in CC the exemplification of the present invention.

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 7; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 15

ABM79007

ID ABM79007 standard; protein; 1356 AA.

AC ABM79007;

XX 15-JAN-2004 (first entry)

XX Human VEGF receptor-2 (KDR).

XX Human; vascular endothelial growth factor receptor-2; VEGFR-2; KDR;
KW receptor; vaccine; genetic immunisation; gene therapy; cytostatic.

XX Homo sapiens.

XX WO2003073995-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006256.

XX 02-MAR-2002; 2002US-00090183.

XX (SCRI) SCRIPPS RES INST.

XX Reisfeld RA, Niethammer AG, Xiang R;

XX WPI; 2003-756753/71.

XX N-PSDB; ACF80601.

XX New DNA vaccine for eliciting an immune response against proliferating
PT endothelial cells comprising a DNA construct operably encoding a VEGF
PT receptor protein in a carrier, useful for inhibiting tumor growth or
PT angiogenesis.

XX Claim 3; Fig 2; 56pp; English.

XX The present sequence is the protein sequence of human vascular
CC endothelial growth factor receptor-2 (VEGFR2 or KDR). A claimed DNA
CC vaccine effective for eliciting an immune response against proliferating
CC endothelial cells comprises a DNA construct operably encoding a VEGF
CC receptor protein (e.g. KDR) in a carrier. The DNA construct may be a
CC naked DNA construct or incorporated into a plasmid vector or into an
CC attenuated bacterial vector such as attenuated Salmonella typhimurium.

CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell
 CC proliferation, inhibiting angiogenesis, and inhibiting tumour growth
 XX
 SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 7; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 16
 ADF45097
 ID ADF45097 standard; protein; 1356 AA.

XX
 AC ADF45097;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human kinase VEGFR2.
 XX
 KW Human; protein kinase; enzyme; inhibitor; VEGFR2.
 XX
 OS Homo sapiens.

XX WO2003081210-A2.
 XX 02-OCT-2003.
 XX
 PF 20-MAR-2003; 2003WO-US008725.
 XX
 PR 21-MAR-2002; 2002US-0366892P.

XX (SUNE-) SUNESIS PHARM INC.

XX Prescott JC, Braisted A;

XX WPI; 2003-865136/80.

XX Identifying ligand binding to inactive conformation of target protein
 PT kinase (T) comprises contacting the conformation modified (T) which
 PT contains reactive group at binding site, with ligands and detecting
 PT kinase-ligand conjugate formation.

XX Disclosure; SEQ ID NO 66; 260pp; English.

XX The present invention relates to a method for identifying a ligand (L),
 CC which binds to an inactive conformation of target protein kinase (T). The
 CC method involves contacting inactive conformation of (T), which contains
 CC or is modified to contain a reactive group at or near a binding site of
 CC interest, with one or more ligand candidates capable of covalently
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
 CC The method is useful for identifying protein kinase inhibitors that
 CC preferentially bind to inactive conformation of a target protein kinase.
 CC The present sequence is a protein kinase which may be modified via an
 CC amino acid substitution, for use in the method of the invention.

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 7; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 17
 ABU64302

ID ABU64302 standard; protein; 1356 AA.
 XX
 AC ABU64302;

XX
 DT 11-MAR-2004 (first entry)

XX Human KDR protein.

XX Vector; rAAV; recombinant adeno-associated viral vector;
 KW anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;
 KW retinal degeneration; macular degeneration; neovascularisation;
 KW ophthalmological.

XX Homo sapiens.

XX WO2003080648-A2.

XX 02-OCT-2003.

XX 20-MAR-2003; 2003WO-US008667.

XX 20-MAR-2002; 2002US-0366114P.

XX (UYFL) UNIV FLORIDA RES FOUND INC.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Hauswirth WM, Campochiaro PA, Berns KI;

XX WPI; 2003-779243/73.

XX N-PSDB; AAL56271.

XX Novel adeno-associated viral vector comprising polynucleotide encoding
 PT pigment epithelium-derived factor, useful for treating choroidal
 PT neovascularization, blindness, loss of vision.

XX Claim 14; Page 50-51; Opp; English.

XX The present invention relates to an adeno-associated viral (AAV) vector
 CC comprising a polynucleotide that comprises a nucleic acid segment that
 CC encodes a choroidal or ocular neovascularisation inhibitory polypeptide
 CC operably linked to a promoter that expresses the segment to produce the
 CC polypeptide in a selected mammalian host cell. Such a vector is useful
 CC for providing a choroidal or ocular neovascularisation inhibitory
 CC polypeptide to a mammal, for use in the therapy of ocular
 CC neovascularisation, choroidal neovascularisation, retinal
 CC neovascularisation, age-related macular degeneration, visual impairment,
 CC ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
 CC The present sequence is a protein shown in the exemplification of the
 CC invention

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 7; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 18

ADH17130

ID ADH17130 standard; protein; 1356 AA.

XX
 AC ADH17130;

XX
 DT 11-MAR-2004 (first entry)

XX Human vascular endothelial growth factor receptor 2 (VEGFR2) protein.

XX tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1;
 KW TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin;

KW vascular endothelial growth factor; VEGF; placental growth factor; PLGF;
KW migration inhibitory factor; MIG; human;
KW vascular endothelial growth factor receptor 2; VEGFR2; receptor.
XX
OS Homo sapiens.
XX WO2003097854-A2.
XX 27-NOV-2003.
XX
XX 19-MAY-2003; 2003WO-US015711.
XX 17-MAY-2002; 2002US-0380872P.
XX 24-FEB-2003; 2003US-0448874P.
XX 24-FEB-2003; 2003US-0448922P.
XX (SUGEN-) SUGEN INC.
XX Morimoto A, Depirimo S, O'farrell A, Smolich BD, Manning WC;
PI Walter SA, Schilling JW, Cherrington J;
XX WPI; 2004-042604/04.
XX
XX Determining whether a test compound inhibits tyrosine kinase activity in
PT a mammal by exposing the mammal to the test compound and measuring in the
PT mammal the level of at least one of the measured proteins or mRNA
PT transcripts.
XX
XX Disclosure; SEQ ID NO 129; 408pp; English.
XX
XX The invention relates to a novel method for determining whether a test
XX compound inhibits tyrosine kinase activity in a mammal comprising
XX measuring in the mammal the level of at least one of the proteins and/or
XX mRNA transcripts or genes for such proteins comprising type 1 plasminogen
XX activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of
XX metalloproteinase 1), vinculin, vascular endothelial growth factor
XX (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or
XX migration inhibitory factor (MIG), exposing the mammal to the test
XX compound and then measuring in the mammal the level of at least one of
XX the proteins and/or mRNA transcripts previously measured. The method of
XX the invention may be useful for determining whether a test compound
XX inhibits tyrosine kinase activity in a mammal. The current sequence is
XX that of the tyrosine kinase activity inhibition-related protein of the
XX invention.
XX
XX Sequence 1356 AA;
SQ
Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 19
ADG70543
ID ADG70543 standard; peptide; 1356 AA.
XX
XX ADG70543;
XX
XX 11-MAR-2004 (first entry)
XX Human KDR/Fik-1, SEQ ID NO:5.
XX Kinase insert domain-containing receptor; foetal liver kinase-1; KDR;
XX Fik-1; KDR/Fik-1; signal transduction inhibition;
XX tyrosine phosphorylation; phosphospecific antibody; transgenic animal;
XX drug screening; tyrosine phosphorylation inhibitor;
XX angiogenesis detection; angiogenesis inhibition; cell growth inhibition;
XX tumour; cancer; diabetic retinopathy; cytostatic; antidiabetic;
XX ophthalmological; human.

XX Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 1214
FT /note= "Tyr is optionally O-phosphorylated"
XX JP2003310276-A.
XX 05-NOV-2003.
XX 30-APR-2002; 2002JP-00129072.
XX 30-APR-2002; 2002JP-00129072.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (SHIB/) SHIBUYA M.
XX WPI; 2004-027148/03.
XX Inhibiting information transmission of kinase insert domain-containing
PT receptor/fms-like tyrosine kinase-1 by a substance that inhibits coupling
PT of information transmission molecules to phosphorylated tyrosines of the
PT kinase.
XX
XX Disclosure; SEQ ID NO 5; 23pp; Japanese.
XX
XX The invention relates to a method of inhibiting signal transduction by
XX kinase insert domain-containing receptor/foetal liver kinase-1 (KDR/Fik-
XX 1) using a substance that inhibits the coupling of a signal transduction
XX molecule to the phosphotyrosine at position 1214 of KDR/Fik-1. The
XX invention also relates to use of KDR/Fik-1 signal transduction inhibitors
XX to inhibit cell growth or angiogenesis; screening for substances which
XX inhibit KDR/Fik-1-mediated signal transduction; the compounds identified;
XX a method of detecting angiogenesis in a tissue; a tyrosine
XX phosphorylation inhibitor that inhibits phosphorylation of tyrosine 1214
XX of KDR/Fik-1; an antibody specific for the phosphorylated form of KDR/Fik
XX -1; a nucleic acid encoding the antibody; and vectors, host cells and
XX transgenic animals comprising the nucleic acid. Inhibition of KDR/Fik-1-
XX mediated signal transduction is useful for inhibiting angiogenesis and
XX cell growth, which is in turn useful in the treatment of diseases such as
XX tumours and diabetic retinopathy. The present sequence represents human
XX KDR/Fik-1.
XX
XX Sequence 1356 AA;
SQ
Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 20
ADQ39806
ID ADQ39806 standard; protein; 1356 AA.
XX
XX ADQ39806;
XX
XX 18-NOV-2004 (first entry)
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1469.
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX Homo sapiens.
XX WO2004058052-A2.
XX 15-JUL-2004.
XX

```
XX PF 22-DEC-2003; 2003WO-US040978.
XX XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX XX
XX PA (APPL-) APPLERA CORP.
XX XX
XX PI Cargill M, Devlin JJ, Iakoubova O;
XX XX
XX DR WPI; 2004-533949/51.
XX DR N-PSDB; ADQ38980.
XX XX
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX XX
XX PS Claim 10; SEQ ID NO 1469; 145pp; English.
XX XX
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNP's of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||
RESULT 21
ADQ39808
ID ADQ39808 standard; protein; 1356 AA.
XX AC ADQ39808;
XX XX
XX DT 18-NOV-2004 (first entry)
XX XX
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1471.
XX XX
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiant; gene therapy; human.
XX XX

OS Homo sapiens.
XX PN WO2004058052-A2.
XX XX
XX PD 15-JUL-2004.
XX XX
XX PF 22-DEC-2003; 2003WO-US040978.
XX XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX XX
XX PA (APPL-) APPLERA CORP.
XX XX
XX PI Cargill M, Devlin JJ, Iakoubova O;
XX XX
XX DR WPI; 2004-533949/51.
XX DR N-PSDB; ADQ38980.
XX XX
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX XX
XX PS Claim 10; SEQ ID NO 1471; 145pp; English.
XX XX
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNP's of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||
RESULT 22
ADR46648
ID ADR46648 standard; protein; 1356 AA.
XX AC ADR46648;
XX XX
XX DT 18-NOV-2004 (first entry)
XX XX
```

DE Cancer-associated protein, SEQ ID 61.
 XX Cytostatic; Gene Therapy; cancer; human.
 XX Homo sapiens.
 OS WO2004073657-A2.
 PN
 XX
 PD 02-SEP-2004.
 XX
 PF 19-FEB-2004; 2004WO-US005455.
 XX
 PR 19-FEB-2003; 2003US-0448784P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Gish KC, Wilson KE, Zlotnik A;
 XX WPI; 2004-652787/63.
 DR N-PSDB; ADR46590.
 XX
 XX Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX
 PS Claim 1; SEQ ID NO 61; 375pp; English.
 XX
 XX The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.
 XX
 SQ Sequence 1356 AA;
 Query Match 100.0%; Score 208; DB 8; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELVEHLGNLQNAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 DB 1154 SELVEHLGNLQNAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
 RESULT 23
 ADT92353
 ID ADT92353 standard; protein; 1356 AA.
 XX
 AC ADT92353;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human vascular endothelial growth factor receptor 2 (VEGFR2) protein.
 XX
 XX vascular endothelial growth factor receptor; VEGFR;
 KW protein co-ordinate data; X-ray diffraction; rational drug design;
 KW VEGFR2.
 XX
 OS Homo sapiens.
 XX
 PN WO2004092217-A1.
 XX
 PD 28-OCT-2004.
 XX
 PF 05-APR-2004; 2004WO-IB001251.
 XX
 PR 17-APR-2003; 2003US-0463957P.
 XX
 XX (PF12) PFIZER INC.
 PA
 XX Bender SL, Kania RS, Mctigue MA, Palmer CL, Pinko C;
 PI Wickersham J;

XX WPI; 2004-784574/77.
 DR N-PSDB; ADT92352.
 XX
 PT Crystalline structure for identifying potential vascular endothelial
 PT growth factor receptor (VEGFR) modulator, of VEGFR peptide and ligand
 PT complex.
 XX
 PS Claim 4; SEQ ID NO 2; 332pp; English.
 XX
 CC This invention relates to the novel crystalline structure of a vascular
 CC endothelial growth factor receptor (VEGFR) peptide-ligand complex, where
 CC the protein co-ordinate data is provided. Specifically, it refers to
 CC using X-ray diffraction techniques to provide structural information
 CC about the VEGFR kinase domain (VEGFRKD) and identify a ligand binding
 CC pocket and activation loop as defined in the specification. The present
 CC invention describes using this information to identify potential VEGFR
 CC modulators, as well as designing potential modulators using rational drug
 CC design and the three-dimensional structural information that will be able
 CC to bind to and modulate the activity of this protein. In particular, it
 CC identifies potentially important atoms and contributory amino acids by
 CC using root mean square deviation to highlight atoms that are within 1.25
 CC Angstroms of the C-alpha core. This polypeptide is the human VEGFR2
 CC protein sequence of the invention.
 XX
 SQ Sequence 1356 AA;
 Query Match 100.0%; Score 208; DB 8; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELVEHLGNLQNAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 DB 1154 SELVEHLGNLQNAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
 RESULT 24
 ADV90285
 ID ADV90285 standard; protein; 1356 AA.
 XX
 AC ADV90285;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Protease-hydrolysed polypeptide #62.
 XX
 KW Protease; immune disorder; inflammation; musculoskeletal disease;
 KW dermatological disease; gastrointestinal disease; endocrine disease;
 KW metabolic disorder; cancer; hematological disease;
 KW cardiovascular disease; neurological disease; neurodegenerative disease;
 KW growth disorder; respiratory disease; genitourinary disease;
 KW gynecological disorder; nutritional disorder; infection; cytostatic;
 KW gastrointestinal-gen.; antidiabetic; antidiabetic; nephrotropic;
 KW antihypertensive; antidiabetic; antidiabetic; antidiabetic;
 KW cardiovascular-gen.; immunosuppressive; respiratory-gen.; antipsoriatic;
 KW antiallergic; dermatological; enzyme; hydrolysis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004113522-A1.
 XX
 PD 29-DEC-2004.
 XX
 PF 18-JUN-2004; 2004WO-EP051173.
 XX
 PR 18-JUN-2003; 2003EP-00013819.
 PR 10-NOV-2003; 2003EP-00025851.
 PR 11-NOV-2003; 2003EP-00025871.
 PR 11-FEB-2004; 2004EP-00003058.
 XX
 XX (DIRE-) DIREVO BIOTECH AG.
 PA
 XX Haupts U, Koltermann A, Scheidig A, Voetsmeier C, Kettling U;

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OM protein - protein search, using sw model

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Title: US-10-763-276-1

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	61.3	365	6 US-10-821-234-1575	Sequence 1575, Ap
2	36	58.1	338	6 US-10-821-234-1565	Sequence 1565, Ap
3	36	58.1	358	6 US-10-821-234-1563	Sequence 1563, Ap
4	34	54.8	322	6 US-10-878-556A-16	Sequence 16, Appl
5	34	54.8	1338	6 US-10-821-234-1622	Sequence 1622, Ap
6	34	54.8	1338	7 US-11-109-156-23	Sequence 23, Appl
7	33	53.2	60	7 US-11-091-668-15	Sequence 15, Appl
8	33	53.2	109	6 US-10-467-657-3702	Sequence 3702, Ap
9	33	53.2	478	6 US-10-467-657-3994	Sequence 3994, Ap
10	33	53.2	772	7 US-11-147-238-2	Sequence 2, Appl
11	33	53.2	772	7 US-11-147-238-5	Sequence 5, Appl
12	33	53.2	1133	6 US-10-821-234-1219	Sequence 1219, Ap
13	32	51.6	214	6 US-10-467-657-7796	Sequence 7796, Ap
14	32	51.6	224	7 US-11-000-463-279	Sequence 279, App
15	32	51.6	234	6 US-10-467-657-2238	Sequence 2238, Ap
16	32	51.6	236	7 US-11-000-463-278	Sequence 278, Ap
17	32	51.6	316	6 US-10-467-657-2250	Sequence 2250, Ap
18	32	51.6	316	6 US-10-467-657-6552	Sequence 6552, Ap
19	32	51.6	319	6 US-10-793-626-2760	Sequence 2760, Ap
20	32	51.6	605	7 US-11-137-465-41	Sequence 41, Appl
21	32	51.6	1683	6 US-10-982-545-6	Sequence 6, Appl
22	31	50.0	114	7 US-11-137-465-52	Sequence 52, Appl
23	31	50.0	182	6 US-10-793-626-2414	Sequence 2414, Ap
24	31	50.0	394	6 US-10-131-826A-520	Sequence 520, App
25	31	50.0	411	6 US-10-793-626-3236	Sequence 3236, App

26	31	50.0	431	7 US-11-060-920-4	Sequence 4, Appli
27	31	50.0	552	6 US-10-793-626-1182	Sequence 1182, Ap
28	31	50.0	718	6 US-10-467-657-8476	Sequence 8476, Ap
29	31	50.0	746	7 US-11-074-176-314	Sequence 314, App
30	31	50.0	747	7 US-11-018-018-1	Sequence 1, Appli
31	31	50.0	747	7 US-11-047-757-1	Sequence 1, Appli
32	31	50.0	749	7 US-11-074-176-54	Sequence 54, Appl
33	31	50.0	944	6 US-10-793-626-3324	Sequence 3324, Ap
34	31	50.0	2828	7 US-11-080-991-54	Sequence 54, Appl
35	31	50.0	2828	7 US-11-186-284-49	Sequence 49, Appl
36	30	48.4	91	6 US-10-467-657-5566	Sequence 5566, Ap
37	30	48.4	245	6 US-10-467-657-4742	Sequence 4742, Ap
38	30	48.4	268	6 US-10-878-556A-46	Sequence 46, Appl
39	30	48.4	311	6 US-10-793-626-3112	Sequence 3112, Ap
40	30	48.4	361	6 US-10-763-712A-122	Sequence 122, App
41	30	48.4	367	6 US-10-793-626-1202	Sequence 1202, Ap
42	30	48.4	379	6 US-10-510-386-76	Sequence 76, Appl
43	30	48.4	382	7 US-11-000-463-447	Sequence 447, App
44	30	48.4	401	7 US-11-110-851-63	Sequence 63, Appl
45	30	48.4	423	7 US-11-110-851-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc SEQ_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 61.3%; Score 38; DB 6; Length 365;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGKDYIVL 9
Db 143 DGKDYIAL 150

RESULT 2
US-10-821-234-1565
; Sequence 1565, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1565
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1565

Query Match 58.1%; Score 36; DB 6; Length 338;
Best Local Similarity 75.0%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
| | | | | | |
Db 143 DGKDYAL 150

RESULT 3

US-10-821-234-1563
; Sequence 1563, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1563
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1563

Query Match 58.1%; Score 36; DB 6; Length 358;
Best Local Similarity 75.0%; Pred. No. 7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
| | | | | | |
Db 140 DGKDYLT 147

RESULT 4

US-10-878-556A-16
; Sequence 16, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/argi_human
; DATABASE ENTRY DATE: 1987-08-13
US-10-878-556A-16

Query Match 54.8%; Score 34; DB 6; Length 322;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLP 10
| | | | | | |
Db 45 CDVKDYGDLP 54

RESULT 5

US-10-821-234-1622
; Sequence 1622, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1622
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1622

Query Match 54.8%; Score 34; DB 6; Length 1338;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYI 7
| | | | |
Db 1165 DGKDYI 1170

RESULT 6

US-11-109-156-23
; Sequence 23, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JF00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-23

Query Match 54.8%; Score 34; DB 7; Length 1338;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYI 7
DB 1165 DGKDYI 1170
|||||

RESULT 7
US-11-091-668-15
; Sequence 15, Application US/11091668
; Publication No. US20050262585A1
; GENERAL INFORMATION:
; APPLICANT: University of Nebraska
; APPLICANT: Mackenzie, Sally Ann
; APPLICANT: Vagchhipawala, Zarir Erach
; TITLE OF INVENTION: Soybean FGAM Synthase Promoters Useful In Parasite Control
; FILE REFERENCE: 1231-221
; CURRENT APPLICATION NUMBER: US/11/091,668
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60556745
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-668-15

Query Match 53.2%; Score 33; DB 7; Length 60;
Best Local Similarity 50.0%; Pred. No. 3.8;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDGKDYIVLP 10
DB 38 CDGRHLAVMP 47
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RESULT 8
US-10-467-657-3702
; Sequence 3702, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3702
; LENGTH: 109
; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3702

Query Match 53.2%; Score 33; DB 6; Length 109;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 11
DB 13 NGADYVIPPI 22
:|||||

RESULT 9
US-10-467-657-3994
; Sequence 3994, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3994
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3994

Query Match 53.2%; Score 33; DB 6; Length 478;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 11
DB 21 DGRDNEVLVP 30
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RESULT 10
US-11-147-238-2
; Sequence 2, Application US/11147238
; Publication No. US20050266534A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, Bettina, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE csta GENE
; FILE REFERENCE: 032301 WD 195
; CURRENT APPLICATION NUMBER: US/11/147,238
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: US/09/935,799
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-147-238-2

Query Match 53.2%; Score 33; DB 7; Length 772;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYI 7
DB 119 DGKDYV 124
|||||

Fri Dec 9 11:55:50 2005

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; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7796
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7796

Query Match      51.6%; Score 32; DB 6; Length 214;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVL 9
      :|:|:|:|
DB      24 EGEDYLV 31

RESULT 14
US-11-000-463-279
; Sequence 279, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-279

Query Match      51.6%; Score 32; DB 7; Length 224;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 CDGKDYIVLPI 11
      :|:|:|:|
DB      214 CPGKRYDAIPL 224

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7796
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7796

Query Match      53.2%; Score 33; DB 7; Length 772;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYI 7
      :|:|:|:|
DB      119 DGKDYV 124

RESULT 12
US-10-821-234-1219
; Sequence 1219, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1219
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1219

Query Match      53.2%; Score 33; DB 6; Length 1133;
Best Local Similarity 40.0%; Pred. No. 87;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 CDGKDYIVLP 10
      :|:|:|:|
DB      435 CDTDDFVMP 444

RESULT 13
US-10-467-657-7796
; Sequence 7796, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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Fri Dec 9 11:55:50 2005

RESULT 15
US-10-467-657-2238
; Sequence 2238, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2238
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2238

Query Match 51.6%; Score 32; DB 6; Length 234;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GKDYIVLP 10
|||:|
Db 179 GKDGVLVP 186

Search completed: December 9, 2005, 10:39:53
Job time : 2.49057 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:24:10 ; Search time 45.8679 Seconds
(without alignments)
100.203 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/us08_PUBCOMB.pep.*
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4: /cgn2_6/prodata/1/pubpaa/us10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	3	US-09-969-037-1 Sequence 1, Appli
2	62	100.0	11	3	US-09-969-037-2 Sequence 2, Appli
3	62	100.0	11	5	US-10-763-276-1 Sequence 1, Appli
4	62	100.0	11	5	US-10-763-276-2 Sequence 2, Appli
5	53	85.5	10	3	US-09-572-404B-4174 Sequence 4174, Ap
6	53	85.5	10	3	US-09-572-404B-4175 Sequence 4175, Ap
7	53	85.5	15	3	US-09-943-382-2 Sequence 2, Appli
8	53	85.5	15	3	US-09-951-265-1 Sequence 1, Appli
9	53	85.5	15	4	US-10-452-786-2 Sequence 2, Appli
10	53	85.5	15	4	US-10-387-355-1 Sequence 1, Appli
11	53	85.5	15	5	US-10-823-995-2 Sequence 2, Appli
12	53	85.5	15	5	US-10-982-543-2 Sequence 2, Appli
13	53	85.5	429	4	US-10-664-421-44 Sequence 44, Appli
14	53	85.5	429	5	US-10-941-635-44 Sequence 44, Appli
15	53	85.5	567	4	US-10-327-414-8 Sequence 8, Appli
16	53	85.5	1306	5	US-10-741-600-1470 Sequence 1470, Ap
17	53	85.5	1354	4	US-10-262-538-30 Sequence 30, Appli
18	53	85.5	1354	4	US-10-669-176-30 Sequence 30, Appli
19	53	85.5	1356	3	US-09-969-037-7 Sequence 7, Appli
20	53	85.5	1356	4	US-10-022-939-2 Sequence 2, Appli
21	53	85.5	1356	4	US-10-100-405A-2 Sequence 2, Appli
22	53	85.5	1356	4	US-10-327-414-6 Sequence 6, Appli
23	53	85.5	1356	4	US-10-090-183-2 Sequence 2, Appli
24	53	85.5	1356	4	US-10-165-193A-11 Sequence 11, Appli
25	53	85.5	1356	4	US-10-394-322A-66 Sequence 66, Appli
26	53	85.5	1356	4	US-10-440-464-129 Sequence 129, App
27	53	85.5	1356	5	US-10-783-528-61 Sequence 61, Appli

28	53	85.5	1356	5	US-10-872-198-115 Sequence 115, App
29	53	85.5	1356	5	US-10-763-276-7 Sequence 7, Appli
30	53	85.5	1356	5	US-10-741-600-1469 Sequence 1469, Ap
31	53	85.5	1356	5	US-10-741-600-1471 Sequence 1471, Ap
32	53	85.5	1356	5	US-10-926-806-10 Sequence 10, Appli
33	53	85.5	1356	5	US-10-824-982-2 Sequence 2, Appli
34	53	85.5	1356	6	US-11-021-951-115 Sequence 115, App
35	50	80.6	1345	4	US-10-090-183-6 Sequence 6, Appli
36	50	80.6	1367	3	US-09-919-408-6 Sequence 2, Appli
37	50	80.6	1367	3	US-09-766-678-2 Sequence 6, Appli
38	50	80.6	1367	3	US-09-872-136-6 Sequence 6, Appli
39	50	80.6	1367	4	US-10-165-193A-10 Sequence 10, Appli
40	50	80.6	1367	5	US-10-639-603-6 Sequence 6, Appli
41	50	80.6	1367	5	US-10-799-782-2 Sequence 2, Appli
42	50	80.6	1367	6	US-11-030-539-6 Sequence 6, Appli
43	47	75.8	136	4	US-10-425-115-363890 Sequence 363890,
44	41.5	66.9	426	5	US-10-471-758-3 Sequence 3, Appli
45	41	66.1	64	4	US-10-424-599-240544 Sequence 240544,

ALIGNMENTS

RESULT 1

US-09-969-037-1
; Sequence 1, Application US/09969037
; Publication No. US2003002247A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/969,037
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Phosphorylation
; LOCATION: 7
; OTHER INFORMATION: an antigen peptide for human KDR/Flk-1 phosphorylated at 1175-
; OTHER INFORMATION: tyrosine corresponding to its residue 1171-1180 and added cyste
; OTHER INFORMATION: residue at the N-terminal
US-09-969-037-1

Query Match 100.0%; Score 62; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDGKDYIVLPI 11
|||||||

Db 1 CDGKDYIVLPI 11
|||||||

RESULT 2

US-09-969-037-2
; Sequence 2, Application US/09969037
; Publication No. US2003002247A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/969,037
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: a peptide consisting of the same sequence as SEQ ID NO:1 without
; US-09-969-037-2 phosphorylation

Query Match      100.0%; Score 62; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 3
US-10-763-276-1
; Sequence 1, Application US/10763276
; Publication No. US20050004003A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits binding of information
; TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/FIk-1
; TITLE OF INVENTION: and usages of the same
; FILE REFERENCE: 249-199
; CURRENT APPLICATION NUMBER: US/10/763.276
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/969,037B
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Phosphorylation
; LOCATION: 7
; FEATURE:
; OTHER INFORMATION: an antigen peptide
US-10-763-276-1

Query Match      100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 4
US-10-763-276-2
; Sequence 2, Application US/10763276
; Publication No. US20050004003A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits binding of information
; TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/FIk-1
; TITLE OF INVENTION: and usages of the same
; FILE REFERENCE: 249-199
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; CURRENT APPLICATION NUMBER: US/10/763.276
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/969,037B
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: a peptide SEQ ID NO:1 without phosphorylation
US-10-763-276-2

Query Match      100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 5
US-09-572-404B-4174
; Sequence 4174, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 4174
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGF at 1169-1178 and may interact wi
; US-09-572-404B-4174 th

Query Match      85.5%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1 DGKDYIVLPI 10

RESULT 6
US-09-572-404B-4175
; Sequence 4175, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 4175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
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; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGP at 1169-1178 and may interact w
; OTHER INFORMATION: Sequence 4174 in this patent.
US-09-572-404B-4175

Query Match      85.5%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1 DGKDYIVLPI 10

RESULT 7
US-09-943-382-2
; Sequence 2, Application US/09943382
; Publication No. US20020103230A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAPER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-943-382-2

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 8
US-09-951-265-1
; Sequence 1, Application US/09951265
; Publication No. US20020107392A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/09/951,265
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: C-term amidated
US-09-951-265-1

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 9
US-10-452-786-2
; Sequence 2, Application US/10452786
; Publication No. US20040002518A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAPER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/452,786
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-452-786-2

Query Match      85.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 10
US-10-387-355-1
; Sequence 1, Application US/10387355
; Publication No. US20040006101A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
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; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/10/387,355
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/951,265
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
; US-10-387-355-1

Query Match 85.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 11

US-10-823-995-2
; Sequence 2, Application US/10823995
; Publication No. US20050137188A1

; GENERAL INFORMATION:
; APPLICANT: RENHOWER, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/823,995
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
; US-10-823-995-2

Query Match 85.5%; Score 53; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 12

US-10-982-543-2
; Sequence 2, Application US/10982543

; Publication No. US20050209247A1
; GENERAL INFORMATION:
; APPLICANT: CAI, SHAOPEI
; APPLICANT: CHOU, JOYCE
; APPLICANT: HARWOOD, ERIC
; APPLICANT: MACHAJEWSKI, TIMOTHY
; APPLICANT: RYCKMAN, DAVID
; APPLICANT: SHANG, XIAO
; APPLICANT: ZHU, SHUGUANG
; TITLE OF INVENTION: PHARMACEUTICALLY ACCEPTABLE SALTS OF QUINOLINONE
; FILE REFERENCE: 072121-0440
; CURRENT APPLICATION NUMBER: US/10/982,543
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/546,017
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/526,425
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/526,426
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/517,915
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
; US-10-982-543-2

Query Match 85.5%; Score 53; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 13

US-10-664-421-44
; Sequence 44, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIVAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-664-421-44

Query Match 85.5%; Score 53; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 9, 2005, 10:39:35
Job time : 46.8679 secs

QY 2 DGKDYIVLPI 11
Db 388 DGKDYIVLPI 397

RESULT 14
US-10-941-635-44
; Sequence 44, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-44

Query Match 85.5%; Score 53; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 388 DGKDYIVLPI 397

RESULT 15
US-10-327-414-8
; Sequence 8, Application US/10327414
; Publication No. US20030158083A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin G
; TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Function of
; TITLE OF INVENTION: Endothelia Phosphatase
; FILE REFERENCE: 8864M
; CURRENT APPLICATION NUMBER: US/10/327,414
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/355,125
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-414-8

Query Match 85.5%; Score 53; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 382 DGKDYIVLPI 391

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:23:55 ; Search time 13.6981 Seconds
(without alignments)
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Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKYIVLPI 11

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	53	85.5	15	2	US-09-951-265-1 Sequence 1, Appli
2	53	85.5	15	2	US-09-943-382-2 Sequence 2, Appli
3	53	85.5	15	2	US-10-452-786-2 Sequence 2, Appli
4	53	85.5	15	2	US-10-387-355-1 Sequence 1, Appli
5	53	85.5	1356	1	US-08-810-116-8 Sequence 8, Appli
6	53	85.5	1356	1	US-07-930-548A-8 Sequence 8, Appli
7	53	85.5	1356	2	US-09-098-707A-2 Sequence 2, Appli
8	53	85.5	1356	2	US-09-483-539-2 Sequence 2, Appli
9	53	85.5	1356	2	US-09-949-016-6198 Sequence 6198, Ap
10	53	85.5	1356	2	US-10-100-405A-2 Sequence 2, Appli
11	53	85.5	1356	2	US-10-022-939-2 Sequence 2, Appli
12	53	85.5	1456	2	US-09-949-016-9853 Sequence 9853, Ap
13	50	80.6	1367	1	US-07-813-593-4 Sequence 4, Appli
14	50	80.6	1367	1	US-07-977-451-6 Sequence 4, Appli
15	50	80.6	1367	1	US-07-946-507-4 Sequence 4, Appli
16	50	80.6	1367	1	US-08-252-517-6 Sequence 6, Appli
17	50	80.6	1367	1	US-07-306-397A-6 Sequence 6, Appli
18	50	80.6	1367	1	US-08-601-891-6 Sequence 6, Appli
19	50	80.6	1367	1	US-08-443-861-2 Sequence 2, Appli
20	50	80.6	1367	1	US-09-021-324-6 Sequence 6, Appli
21	50	80.6	1367	2	US-08-193-829B-2 Sequence 2, Appli
22	50	80.6	1367	2	US-09-872-136B-6 Sequence 6, Appli
23	50	80.6	1367	2	US-09-766-678-2 Sequence 2, Appli
24	50	80.6	1367	2	US-09-919-408A-6 Sequence 6, Appli
25	50	80.6	1367	4	PCT-US92-02750-8 Sequence 8, Appli
26	50	80.6	1367	4	PCT-US92-05401-6 Sequence 6, Appli
27	50	80.6	1367	4	PCT-US92-09893-6 Sequence 6, Appli

28	40	64.5	115	2	US-08-936-165A-449 Sequence 449, App
29	40	64.5	294	2	US-09-902-540-16818 Sequence 16818, A
30	38	61.3	14	2	US-08-914-372C-16 Sequence 16, Appl
31	38	61.3	92	2	US-09-673-809-25 Sequence 25, Appl
32	38	61.3	92	2	US-09-673-809-104 Sequence 104, App
33	38	61.3	92	2	US-09-673-809-106 Sequence 106, App
34	38	61.3	156	2	US-09-513-999C-4289 Sequence 4289, Ap
35	38	61.3	181	2	US-09-013-077A-13 Sequence 13, Appl
36	38	61.3	182	1	US-08-127-954-135 Sequence 135, App
37	38	61.3	182	1	US-08-127-954-136 Sequence 136, App
38	38	61.3	182	1	US-08-127-954-137 Sequence 137, App
39	38	61.3	182	1	US-08-127-954-138 Sequence 138, App
40	38	61.3	182	1	US-08-127-954-139 Sequence 139, App
41	38	61.3	182	1	US-08-127-954-140 Sequence 140, App
42	38	61.3	182	1	US-08-127-954-141 Sequence 141, App
43	38	61.3	182	1	US-08-127-954-142 Sequence 142, App
44	38	61.3	182	1	US-08-127-954-143 Sequence 143, App
45	38	61.3	182	1	US-08-127-954-144 Sequence 144, App

ALIGNMENTS

RESULT 1
US-09-951-265-1
; Sequence 1, Application US/09951265
; Patent No. 6605617
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAFER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/09/951,265
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-951-265-1

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
|||||
Db 6 DGKDYIVLPI 15

RESULT 2
US-09-943-382-2
; Sequence 2, Application US/09943382
; Patent No. 6756383
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN

; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-943-382-2

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 3
US-10-452-786-2
; Sequence 2, Application US/10452786
; Patent No. 6759417
; GENERAL INFORMATION:
; APPLICANT: RENHOM, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/452,786
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-452-786-2

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 4
US-10-387-355-1
; Sequence 1, Application US/10387355
; Patent No. 6762194

; GENERAL INFORMATION:
; APPLICANT: RENHOM, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/10/387,355
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/951,265
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-387-355-1

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 5
US-08-810-116-8
; Sequence 8, Application US/08810116
; Patent No. 5766860
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5766860a1 Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/810,116
; APPLICATION NUMBER: US/08/810,116
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/930,548
; FILING DATE: 23-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-116-8

Query Match      85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 6
US-07-930-548A-8
; Sequence 8, Application US/07930548A
; Patent No. 5861301
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5861301el Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-930-548A-8

Query Match      85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 7
US-09-098-707A-2
; Sequence 2, Application US/09098707A
; Patent No. 6204011
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;
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew J.
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Jun-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19963PV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-098-707A-2

Query Match      85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 8
US-09-483-539-2
; Sequence 2, Application US/09483539
; Patent No. 6359115
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew J.
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,539
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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19963pv
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-483-539-2

Query Match 85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1171 DGKDYIVLPI 1180

RESULT 9
US-09-949-016-6198
; Sequence 6198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6198
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6198

Query Match 85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1171 DGKDYIVLPI 1180

RESULT 10
US-10-100-405A-2
; Sequence 2, Application US/10100405A
; Patent No. 6811367
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDC
; CURRENT APPLICATION NUMBER: US/10/100,405A
; CURRENT FILING DATE: 2002-08-13
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; PRIOR APPLICATION NUMBER: 10/022,939
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-100-405A-2

Query Match 85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1171 DGKDYIVLPI 1180

RESULT 11
US-10-022-939-2
; Sequence 2, Application US/10022939
; Patent No. 6841382
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2

Query Match 85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1171 DGKDYIVLPI 1180

RESULT 12
US-09-949-016-9853
; Sequence 9853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9853
;; LENGTH: 1456
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-9853

Query Match 85.5%; Score 53; DB 2; Length 1456;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
|||||||
Db 1271 DGKDYIVLPI 1280

RESULT 13
US-07-813-593-4
; Sequence 4, Application US/07813593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 19920415
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-813-593-4

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. No. 1.5;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DGKDYIVLPI 11
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Db 1169 DGKDYIVLPM 1178
RESULT 14
US-07-977-451-6
; Sequence 6, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-451-6

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. NO. 1.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1169 DGKDYIVLPM 1178

RESULT 15

US-07-946-507-4
; Sequence 4, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946.507
; FILING DATE: 19920917
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/813.593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/793.065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/728.913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/679.666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-946-507-4

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. NO. 1.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1169 DGKDYIVLPM 1178

Search completed: December 9, 2005, 10:35:48
Job time : 13.6981 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:19:24 ; Search time 57.4906 Seconds
(without alignments)
84.069 Million cell updates/sec

Title: US-10-763-276-1

Perfect score: 62

Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	5	Aau79424 Human KDR
2	53	85.5	10	4	Aag97980 Human com
3	53	85.5	10	4	Aag97979 Human com
4	53	85.5	10	9	Ady85472 Catalytic
5	53	85.5	1306	8	Adq39807 Human myo
6	53	85.5	1354	9	Adz00446 VEGFR-2.
7	53	85.5	1355	2	Aaw80997 Human rec
8	53	85.5	1356	2	Aar26999 Novel typ
9	53	85.5	1356	2	Aaw59275 Human KDR
10	53	85.5	1356	4	Aab62475 Human VEG
11	53	85.5	1356	4	Aay97783 Human KDR
12	53	85.5	1356	4	Aay97576 Human Flk
13	53	85.5	1356	5	Aau79427 Human Kin
14	53	85.5	1356	5	Aau79429 Human Kin
15	53	85.5	1356	5	Aau79426 Human Kin
16	53	85.5	1356	6	Abra40196 Human vas
17	53	85.5	1356	7	Add08954 Human VEG
18	53	85.5	1356	7	Abm79007 Human VEG
19	53	85.5	1356	7	Adf45097 Human kin
20	53	85.5	1356	7	Abu64302 Human KDR
21	53	85.5	1356	8	Adhl7130 Human vas
22	53	85.5	1356	8	Adg70543 Human KDR
23	53	85.5	1356	8	Adq39806 Human myo
24	53	85.5	1356	8	Adq39808 Human myo

25	53	85.5	1356	8	ADR46648	Adr46648 Cancer-as
26	53	85.5	1356	8	ADT92353	Adt92353 Human vas
27	53	85.5	1356	9	ADY90285	Ady90285 Protease-
28	53	85.5	1356	9	ADY59385	Ady59385 Human VEG
29	53	85.5	1356	9	ADZ26561	Adz26561 Human VEG
30	50	80.6	558	8	ADR32352	Adr32352 Rat recep
31	50	80.6	820	8	ADR32354	Adr32354 GST-rat K
32	50	80.6	1343	8	ADR32351	Adr32351 Rat recep
33	50	80.6	1343	8	ADR32338	Adr32338 Rat Optim
34	50	80.6	1345	7	ABM79009	Abm79009 Murine Fl
35	50	80.6	1367	2	AAR28041	Aar28041 flk-1. 3/
36	50	80.6	1367	2	AAR31377	Aar31377 Human flk
37	50	80.6	1367	2	AAR37504	Aar37504 Murine fl
38	50	80.6	1367	2	AAR44996	Aar44996 Murine fl
39	50	80.6	1367	2	AAR54046	Aar54046 Sequence
40	50	80.6	1367	2	AAR67537	Aar67537 Mouse flk
41	50	80.6	1367	2	AAR67817	Aar67817 Flk1 rece
42	50	80.6	1367	2	AAR97420	Aar97420 Murine fo
43	50	80.6	1367	2	AAW19875	Aaw19875 Murine fl
44	50	80.6	1367	2	ADP90725	Adp90725 Mouse foe
45	50	80.6	1367	2	AAy08618	Aay08618 Murine fl

ALIGNMENTS

RESULT 1

AAU79424

ID AAU79424 standard; peptide; 11 AA.

XX AC AAU79424;

XX DT 02-JUL-2002 (first entry)

XX DE Human KDR/FLK-1 phosphorylated antigenic peptide.

XX KW Human; KDR; kinase insert domain-containing receptor; FLK-1;

XX KW fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic;

XX KW antiarthritic; signal transduction; phosphorylation; cell proliferation;

XX KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis;

XX KW immunogen.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide

FT Modified-site

FT /note= "Non-human added C terminal Cys"

FT /label= OTHER

FT /note= "Tyr is optionally phosphorylated"

WO200229090-A1.

11-APR-2002.

02-OCT-2001; 2001WO-JP008684.

03-OCT-2000; 2000JP-00303694.

(KYOW) KYOWA HAKKO KOGYO KK.

(SHIBU) SHIBUYA M.

Shibuya M, Takahashi T, Furuya A, Shitara K;

WPI; 2002-352237/38.

Screening substances inhibiting the binding of signal-transducing molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as cell proliferation inhibitors and angiogenesis inhibitors for treatment of e.g., tumor.

Example 1; Page 63; 81pp; Japanese.

XX The invention relates to inhibiting the signal transduction of KDR/Flk-1
 CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
 CC using a substance inhibiting the binding of a signal-transducing molecule
 CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
 CC included are methods of detecting/inhibiting/screening for cell
 CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
 CC phosphorylation at tyrosine at the 1175-position using the binding
 CC inhibitors, compounds obtained by the screening methods, drugs containing
 CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-1
 CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
 CC monoclonal antibody or its fragment, a recombinant vector containing the
 CC DNA and a transformant obtained by transferring the recombinant vector
 CC into a host cell. The method is useful for screening substances
 CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
 CC phosphorylated at tyrosine at 1175-position, as cell proliferation
 CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
 CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
 CC detecting angiogenesis is also provided. The present sequence is a
 CC peptide based on residues 1171-1180 of KDR/FLK-1 used to generate
 CC antibodies against the 1175-position phosphorylated KDR/FLK-1
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00036; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;

Qy 1 CDGKDYIVLPI 11
 |||||
 Db 1 CDGKDYIVLPI 11

RESULT 2
 AAG97980
 ID AAG97980 standard; peptide; 10 AA.

XX AC AAG97980;
 XX
 XX 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 4175.
 XX Human; complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.
 XX WO200142277-A2.
 XX PD 14-JUN-2001.
 XX PF 13-DEC-2000; 2000WO-GB004776.
 XX PR 13-DEC-1999; 99GB-00029464.
 XX PA (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;
 XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX Example 6; Page 631; 646pp; English.

XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided

CC in the specification
 XX Sequence 10 AA;

Query Match 85.5%; Score 53; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
 |||||
 Db 1 DGKDYIVLPI 10

RESULT 3
 AAG97979
 ID AAG97979 standard; peptide; 10 AA.

XX AC AAG97979;
 XX
 DT 18-SEP-2001 (first entry)
 XX Human complementary peptide, SEQ ID NO: 4174.
 DE Human; complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.
 XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004776.
 XX PR 13-DEC-1999; 99GB-00029464.

XX PA (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX Example 6; Page 631; 646pp; English.

XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided

XX in the specification

XX Sequence 10 AA;
 Query Match 85.5%; Score 53; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
 |||||
 Db 1 DGKDYIVLPI 10

RESULT 4
 ADY85472
 ID ADY85472 standard; protein; 429 AA.

XX AC ADY85472;
 XX
 DT 16-JUN-2005 (first entry)

XX Catalytic domain of PIM kinase-like protein VEGFR.
DE Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
XX neoplasm; inflammation; antiinflammatory.
KW Unidentified.
XX WO2005028624-A2.
XX
XX 31-MAR-2005.
XX 15-SEP-2004; 2004WO-US030360.
XX 15-SEP-2003; 2003US-0503277P.
XX (PLEX-) PLEXIKON INC.
XX Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX WPI; 2005-273155/28.
XX
XX New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
XX Disclosure; Page 170-174; 236pp; English.
XX
XX The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII)), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group), and developing a ligand for a kinase
CC comprising conserved residues matching at least one of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease

CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
XX Sequence 429 AA;
SQ
Query Match 85.5%; Score 53; DB 9; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKDYIVLPI 11
| | | | | | | | | |
DB 388 DGKDYIVLPI 397
| | | | | | | | | |
RESULT 5
ADQ39807
ID ADQ39807 standard; protein; 1306 AA.
XX
XX AC ADQ39807;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1470.
XX
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX OS Homo sapiens.
XX
XX PN WO2004058052-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 22-DEC-2003; 2003WO-US040978.
XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX
XX PR 10-MAR-2003; 2003US-0453135P.
XX
XX PR 30-APR-2003; 2003US-0466412P.
XX
XX PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JU, Iakubova O;
XX
XX WPI; 2004-533949/51.
XX
XX N-PSDB; ADQ38979.
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1470; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification, an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1306 AA;

Query Match 85.5%; Score 53; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
 |||||
 Db 1121 DGKDYIVLPI 1130

RESULT 6
 ADZ00446
 ID ADZ00446 standard; protein; 1354 AA.

XX AC ADZ00446;

XX 16-JUN-2005 (first entry)

XX VEGFR-2.

XX VEGF-C agonist; VEGF-D agonist; Nootropic; Neuroprotective;
 KW Antiparkinsonian; Anticonvulsant; CNS-Gen.; Antiinflammatory; Anti-HIV;
 KW Virucide; Vasotropic; vascular endothelial growth factor C; VEGF-C;
 KW vascular endothelial growth factor D; VEGF-D; recruitment; proliferation;
 KW differentiation; migration; survival; neural cell; precursor; VEGFR-3;
 KW neuropilin-2; VEGF-C deltaC156; heparin-binding VEGF-C;
 KW neurotherapeutic; interferon gamma; nerve growth factor;
 KW epidermal growth factor; EGF; basic fibroblast growth factor; bFGF;
 KW neurogenin; brain derived neurotrophic factor; BDNF; thyroid hormone;
 KW bone morphogenic protein; BMP; leukemia inhibitory factor; LIF;
 KW sonic hedgehog; glial cell line-derived neurotrophic factor; GDNF;
 KW vascular endothelial growth factor; VEGF; interleukin; interferon;
 KW stem cell factor; SCF; activin; inhibin; chemokine; retinoic acid;
 KW ciliary neurotrophic factor; CNTF; tacrine; Cognex; donepezil; Aricept;
 KW rivastigmine; Exelon; galantamine; Reminyl; cholinesterase inhibitor;
 KW anti-inflammatory; anti-cholinergic; dopamine agonist;
 KW catechol-0-methyl-transferase; COMT; amantadine; Symmetrel; Sinemet;
 KW Selegiline; carbidopa; ropinirole; Requip; coenzyme Q10; Pramipexole;
 KW Mirapex; levodopa; L-dopa; Alzhemers disease; Parkinsons disease;
 KW Huntingtons disease; motor neuron disease;
 KW Amylotrophic Lateral Sclerosis; ALS; dementia; cerebral palsy;
 KW demyelination; multiple sclerosis; phenylketonuria;
 KW periventricular leukomalacia; PVL; HIV-1 encephalitis; HIVE;
 KW Guillian Barre Syndrome; GBS;
 KW acute inflammatory demyelinating polynuropathy; AIDP;
 KW acute motor axonal neuropathy; AMAN;
 KW acute motor sensory axonal neuropathy; AMSAN; Fisher syndrome;
 KW acute pandysautonomia;
 KW chronic inflammatory demyelinating polyradiculoneuropathy; CIDP;
 KW multifocal acquired demyelinating sensory and motor neuropathy; MADSAM;
 KW Lewis-Sumner syndrome;
 KW distal acquired demyelinating symmetric neuropathy; DADS; neural trauma;
 KW neural injury; stroke; spinal cord injury; post-operative injury;
 KW brain ischemia; neuroblastoma; neural tumor.

OS Homo sapiens.

XX WO2005030240-A2.

XX 07-APR-2005.
 XX PD 23-SEP-2004; 2004WO-US031318.
 XX PF 23-SEP-2003; 2003US-00669176.
 XX PR 23-SEP-2003; 2003US-0505607P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX (LICN) LICENTIA LTD.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Alitalo K, Karkkainen M, Haiko P, Sainio K, Wartiovaara K;
 XX Thomas JL, Eichmann A;
 XX WPI; 2005-273287/28.
 XX N-PSDB; ADZ00445.
 XX GENBANK; L04947.
 XX Use of a vascular endothelial growth factor-C or -D product in
 PT medicaments for promoting growth and differentiation of neural stem cells
 PT for neurodegenerative disorders such as Alzheimer's and Parkinson's
 PT disease.
 XX Disclosure; SEQ ID NO 28; 263pp; English.
 XX This sequence represents VEGFR-2. The method of the invention uses a
 CC vascular endothelial growth factor-C (VEGF-C) product or a vascular
 CC endothelial growth factor D (VEGF-D) product in the manufacture of a
 CC medicament to promote recruitment, proliferation, differentiation,
 CC migration or survival of neural cells or neural precursor cells. The
 CC method of the invention comprises identifying a mammalian subject in need
 CC of treatment to promote recruitment, proliferation, differentiation,
 CC migration, or survival of neural cells or neural precursor cells, and
 CC administering to the subject a composition comprising a VEGF-C or VEGF-D
 CC product. The product is a VEGF-C product comprising a purified mammalian
 CC prepro-VEGF-C polypeptide or its fragment that binds VEGFR-3 or
 CC neuropilin-2, a VEGF-C deltaC156 polypeptide, or a chimeric heparin-
 CC binding VEGF-C polypeptide. The method also comprises administering to
 CC the mammalian subject a neurotherapeutic agent, and including in the
 CC medicament a neurotherapeutic agent. The neurotherapeutic agent comprises
 CC a neural growth factor and/or a polynucleotide encoding a neural growth
 CC factor selected from interferon gamma, nerve growth factor, epidermal
 CC growth factor (EGF), basic fibroblast growth factor (bFGF), neurogenin,
 CC brain derived neurotrophic factor (BDNF), thyroid hormone, bone
 CC morphogenic proteins (BMPs), leukemia inhibitory factor (LIF), sonic
 CC hedgehog, glial cell line-derived neurotrophic factor (GDNF), vascular
 CC endothelial growth factor (VEGF), interleukins, interferons, stem cell
 CC factor (SCF), activins, inhibins, chemokines, retinoic acid and ciliary
 CC neurotrophic factor (CNTF). The neurotherapeutic agent is also tacrine
 CC (Cognex), donepezil (Aricept), rivastigmine (Exelon), galantamine
 CC (Reminyl), cholinesterase inhibitors or anti-inflammatory drugs, and/or
 CC is anti-cholinergics, dopamine agonists, catechol-0-methyl-transferases
 CC (COMTs), amantadine (Symmetrel), Sinemet (RTM), Selegiline, carbidopa,
 CC ropinirole (Requip), coenzyme Q10, Pramipexole (Mirapex) and levodopa (L-
 CC dopa). The medicament of the invention is for the treatment of a disease
 CC or condition characterized by aberrant growth of neuronal cells, neuronal
 CC scarring, or neurodegeneration, or for treatment of neural degeneration
 CC caused by a neurodegenerative disorder selected from the group consisting
 CC of is Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC motor neuron disease, Amylotrophic Lateral Sclerosis (ALS), dementia and
 CC cerebral palsy, and for treatment of a disease or condition with aberrant
 CC growth of oligodendrocyte or oligodendrocyte precursor cells, where the
 CC condition has demyelination in the nervous system. The medicament is also
 CC for the treatment of multiple sclerosis, phenylketonuria, periventricular
 CC leukomalacia (PVL), HIV-1 encephalitis (HIVE), Guillian Barre Syndrome
 CC (GBS), acute inflammatory demyelinating polynuropathy (AIDP), acute
 CC motor axonal neuropathy (AMAN), acute motor sensory axonal neuropathy
 CC (AMSAN), Fisher syndrome, acute pandysautonomia, and Krabbe's disease.
 CC The medicament can also be used for the treatment of chronic inflammatory
 CC demyelinating polyradiculoneuropathy (CIDP), such as multifocal acquired
 CC demyelinating sensory and motor neuropathy (MADSAM, also know as Lewis-
 CC Sumner syndrome) and distal acquired demyelinating symmetric neuropathy

CC (DADS), and for the treatment of neural trauma or neural injury, where
 CC the neural trauma is a stroke-related injury, spinal cord injury, post-
 CC operative injury or brain ischemia. The VEGF-C inhibitor is useful in the
 CC manufacture of a medicament for the treatment of a neuroblastoma or
 CC neural tumor. The methods and compositions of the present invention are
 CC also useful for cellular and molecular biology and medicine, in
 CC particular for the vascularization and angiogenesis and the interactions
 CC of the vascular system with the nervous system.

XX Sequence 1354 AA;

Query Match 85.5%; Score 53; DB 9; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
 |||||
 DB 1169 DGKDYIVLPI 1178

RESULT 7

ID AAW80997 standard; protein; 1355 AA.

XX AAW80997;

XX 12-APR-1999 (first entry)

XX Human receptor tyrosine kinase KDR.

XX KDR; receptor tyrosine kinase; human; signal transduction; mitogen;
 KW neangiogenesis; angiogenesis; diabetic retinopathy; breast cancer;
 KW brain cancer; inflammation; rheumatoid arthritis; psoriasis;
 KW contact dermatitis; hypersensitivity; antagonist; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 780..1386
 FT /note= "intracellular domain, from about amino acid 780-
 FT 795 to about amino acid 1175-1386"

XX WO9858053-A1.

XX 23-DEC-1998.

XX 17-JUN-1998; 98WO-US012569.

XX 18-JUN-1997; 97US-0050962P.

XX (MERI) MERCK & CO INC.

XX Kendall RL, Thomas KA, Mao X, Tebben A;

XX WPI; 1999-095333/08.

XX N-PSDB; AAV99829.

XX Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for
 FT antagonists useful to treat diseases involving neangiogenesis e.g.
 FT diabetic retinal vascularization, cancers.

XX Claim 2; Fig 2; 69pp; English.

XX This is the amino acid sequence of a novel receptor tyrosine kinase,
 CC termed KDR, that is expressed on human endothelial cells. KDR is
 CC activated by vascular endothelial growth factor and mediates a mitogenic
 CC signal. It is implicated in clinical neangiogenesis. The amino acid
 CC sequence was deduced from an isolated KDR cDNA (see AAV99829). The
 CC predicted sequence has differences from the previously published KDR
 CC sequence at positions 498 (Ala to Glu), 772 (Thr to Ala), 787 (Gly to
 CC Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Thr to Ser), producing
 CC a protein predicted by computer modeling to have higher activity and
 CC functionality. The invention also relates to recombinant vectors and

CC recombinant hosts which contain a DNA fragment encoding human KDR, a DNA
 CC fragment encoding the intracellular portion of KDR with or without a
 CC membrane anchor sequence, purified forms of associated human KDR, and
 CC human mutant forms of KDR. KDR, fusion proteins or fragments can be used
 CC in assays to identify antagonists and agonists of human KDR (claimed).
 CC Antagonists of KDR useful for treating diseases involving neangiogenesis
 CC e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.)
 CC and forms of inflammation e.g. rheumatoid arthritis, psoriasis, contact
 CC dermatitis and hypersensitivity reactions. The protein is also useful for
 CC produce antibodies that can be used to measure human KDR levels and/or
 CC activity

XX Sequence 1355 AA;

Query Match 85.5%; Score 53; DB 2; Length 1355;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
 |||||
 DB 1170 DGKDYIVLPI 1179

RESULT 8

AAR26999

ID AAR26999 standard; protein; 1356 AA.

XX AAR26999;

XX 23-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX Novel type III RTK encode by the KDR gene.

XX Receptor tyrosine kinase; vascular endothelial cell growth factors;
 KW cancer; tumour; diagnosing; monitoring.

XX Homo sapiens.

XX Unidentified.

XX Key Location/Qualifiers

FT Domain 1..763
 FT /note= "putative extracellular region - contains 21
 FT cysteine residues"

FT Modified-site 46

FT /note= "potential N linked glycosylation site"

FT Modified-site 66

FT /note= "potential N-linked glycosylation site"

FT Modified-site 96

FT /note= "potential N-linked glycosylation site"

FT Modified-site 143

FT /note= "potential N-linked glycosylation site"

FT Modified-site 158

FT /note= "potential N-linked glycosylation site"

FT Modified-site 245

FT /note= "potential N-linked glycosylation site"

FT Modified-site 318

FT /note= "potential N-linked glycosylation site"

FT Modified-site 374

FT /note= "potential N-linked glycosylation site"

FT Modified-site 395

FT /note= "potential N-linked glycosylation site"

FT Modified-site 511

FT /note= "potential N-linked glycosylation site"

FT Modified-site 523

FT /note= "potential N-linked glycosylation site"

FT Modified-site 580

FT /note= "potential N-linked glycosylation site"

FT Modified-site 613

FT /note= "potential N-linked glycosylation site"

FT Modified-site 631

FT /note= "potential N-linked glycosylation site"

PS Claim 1; Fig 7A-M; 51pp; English.

CC This sequence represents a novel human growth factor receptor, kinase

CC insert domain containing receptor or KDR. This receptor is capable of

CC binding to the vascular endothelial cell growth factor, VEGF and is used

CC in a screening assay which identifies compounds that inhibit VEGF action

CC on KDR. Such compounds which inhibit binding of VEGF to the KDR may

CC inhibit angiogenesis and thus be useful for treating cancer

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 2; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 10

AA62475

ID AAB62475 standard; protein; 1356 AA.

XX

XX AAB62475;

XX

XX 09-JUL-2001 (first entry)

DT Human VEGFR-2 receptor protein.

DE

DE Human VEGFR-2 receptor protein.

XX

XX Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2;

KW neuropilin-1; NP-1; co-receptor; human; angiogenic.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH Domain 1..760

FT /note= "extracellular domain"

FT Domain 124..320

FT /note= "Ig domain"

XX

XX WO200131346-A2.

PN

XX 03-MAY-2001.

PD

XX 26-OCT-2000; 2000WO-US029579.

PF

XX 28-OCT-1999; 99US-0162367P.

PR

XX (PROC) PROCTER & GAMBLE CO.

PA

XX Rosenbaum JS, Whitaker GB, Limberg BJ;

PI WPI; 2001-308686/32.

XX

XX N-PSDB; AAF83308.

DR

XX

XX Determining compounds which bind to a complex comprising vascular

FT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior

PT pro- and anti-angiogenic agents.

PT

XX Claim 7; Page 32-39; 82pp; English.

PS

XX The invention relates to determining whether a compound is capable of

CC binding to a receptor protein complex comprising a vascular endothelial

CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1

CC (NP-1) receptor protein. One method comprises introducing a sample

CC comprising the compound to the receptor protein and allowing the compound

CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the

CC presence of the NP-1 co-receptor. The methods of the invention can be

CC used for identifying novel pro- and anti-angiogenic compounds. The

CC present sequence represents the human VEGFR-2 receptor protein

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 4; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 11

AA97783

ID AAY97783 standard; protein; 1356 AA.

XX

XX AAY97783;

XX

XX 22-AUG-2001 (first entry)

DT Human KDR/Flk-1 protein.

DE

DE Immunoglobulin-like domain; Ig-like domain; retinal neovascularisation;

XX

XX vascular endothelial growth factor receptor; VEGF receptor; inflammation;

KW psoriasis; rheumatoid arthritis; haemangioma; leiomyoma; angiofibroma;

KW

XX diabetic retinopathy; endometriosis; macular degeneration; cancer;

KW

XX dimerisation inhibitor; therapy; KDR/Flk-1; human.

XX

XX Homo sapiens.

OS

XX WO200142284-A2.

PN

XX 14-JUN-2001.

PD

XX 07-DEC-2000; 2000WO-GB004693.

PF

XX 07-DEC-1999; 99GB-00028950.

PR

XX (METR-) METRIS THERAPEUTICS LTD.

PA

XX Pappa H;

PI

XX WPI; 2001-381631/40.

DR

XX

XX Novel proteins that prevent dimerization of vascular endothelial growth

PT factor receptors and for treating diseases in which the receptor plays a

PT role e.g. inflammation, cancer, diabetic retinopathy, psoriasis.

PT

XX Claim 11; Fig 3; 83pp; English.

PS

XX This sequence represents the human KDR/Flk-1 protein. The invention

CC relates to a protein comprising the amino acid sequence of the fourth

CC immunoglobulin (Ig)-like domain of a vascular endothelial growth factor

CC (VEGF) receptor or a variant of the protein that retains the ability to

CC bind to a VEGF receptor. The protein, its functional equivalent and DNA

CC encoding it are useful for treating a disorder whose pathology is

CC dependent upon a VEGF family-mediated pathway, including inflammation,

CC psoriasis, rheumatoid arthritis, haemangiomas, leiomyomas, diabetic

CC retinopathy, angiofibromas, endometriosis, macular degeneration, retinal

CC neovascularisation or cancer. The protein or its functional equivalents

CC are also useful for inhibiting the dimerisation of a VEGF receptor

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 4; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 12

AA97576

```

ID XX AA97576 standard; protein; 1356 AA.
XX AC
XX AC AA97576;
XX DT
XX DT 05-APR-2001 (first entry)
XX DE Human Flk-1 transmembrane and extracellular domains.
XX KW Human; angiogenic protein; wound healing; vascular tissue repair;
XX KW peripheral arterial disease; critical limb ischaemia; coronary disease;
XX KW angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
XX KW rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
XX KW infectious disease; neurodegeneration; Flk-1.
XX OS
XX OS Homo sapiens.
XX PN WO200075163-A1.
XX PD 14-DEC-2000.
XX PF 01-JUN-2000; 2000WO-US014925.
XX PR 03-JUN-1999; 99US-0137796P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM, Hu J, Cao L;
XX DR WPI; 2001-071057/08.
XX PT New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
XX PT healing of wounds and treating peripheral arterial disease, critical limb
XX PT ischemia or coronary disease.
XX PS
XX PS Example 48; Page 236-240; 244pp; English.
XX CC This sequence is a human Flk-1 fragment, and was used in the isolation of
XX CC an angiogenic protein of the invention. The angiogenic proteins and the
XX CC DNA sequences encoding them, are used to prevent, treat or ameliorate
XX CC disease and to detect diseases, or susceptibility, by detecting mutations
XX CC or the presence or amount of angiogenic protein expression. Particularly
XX CC they are used to stimulate wound healing, growth of damaged bone and
XX CC tissue, and for repair of vascular tissue, especially peripheral arterial
XX CC disease, critical limb ischaemia or coronary disease. Antagonists of the
XX CC sequences are used to inhibit angiogenesis in tumours and to treat
XX CC inflammation (where associated with increased vascular permeability),
XX CC diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are
XX CC also useful for stimulating (lymph)angiogenesis. The proteins are also
XX CC used to identify specific binding agents (potential therapeutic agents)
XX CC and to raise antibodies. The antibodies are useful as therapeutic
XX CC (ant)agonists; for detection, purification and targeting of proteins for
XX CC in vivo or in vitro diagnosis (including imaging) or for therapy
XX CC (including when linked to e.g. a label or cytotoxin); and for
XX CC immunotyping of cells, e.g. for detecting minimal residual disease or
XX CC haematopoietic progenitor/stem cells. It is also contemplated that the
XX CC sequences might be useful for treating a very wide range of other
XX CC disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases
XX CC (viral, bacterial, fungal or parasitic); neurodegeneration, also as
XX CC chemotactic agents or for stimulating regeneration of the nervous system
XX CC etc
XX SQ Sequence 1356 AA;
Query Match 85.5%; Score 53; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKDIVLPI 11
Db 1171 DGKDIVLPI 1180
RESULT 13

```

```

AAU79427
ID AAU79427 standard; protein; 1356 AA.
XX AC
XX AC AAU79427;
XX DT
XX DT 02-JUL-2002 (first entry)
XX DE Human Kinase insert domain-containing receptor mutant Y801F.
XX KW Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
XX KW fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic; muten;
XX KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
XX KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX OS
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Misc-difference 801 /note= "Wild-type Tyr substituted by Phe"
XX FT
XX PN WO200229090-A1.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-JP008684.
XX PR 03-OCT-2000; 2000JP-00303694.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA (SHIB/) SHIBUYA M.
XX PI Shibuya M, Takahashi T, Furuya A, Shitara K;
XX DR WPI; 2002-352237/38.
XX CC Screening substances inhibiting the binding of signal-transducing
XX CC molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
XX CC cell proliferation inhibitors and angiogenesis inhibitors for treatment
XX CC of e.g. tumor.
XX PS
XX PS Example 8; Page; 81pp; Japanese.
XX CC The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
XX CC using a substance inhibiting the binding of a signal-transducing molecule
XX CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
XX CC included are methods of detecting/inhibiting/screening for cell
XX CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
XX CC phosphorylation at tyrosine at the 1175-position using the binding
XX CC inhibitors, compounds obtained by the screening methods, drugs containing
XX CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk
XX CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
XX CC monoclonal antibody or its fragment, a recombinant vector containing the
XX CC DNA and a transformant obtained by transferring the recombinant vector
XX CC into a host cell. The method is useful for screening substances
XX CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
XX CC phosphorylated at tyrosine at 1175-position, as cell proliferation
XX CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
XX CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
XX CC detecting angiogenesis is also provided. The present sequence is the
XX CC Human KDR/FLK-1 mutant where Tyr at 801 is replaced by Phe. Note: The
XX CC present sequence is not shown in the specification but was created by the
XX CC indexer using the KDR/FLK-1 sequence appearing as AAU74926 and the
XX CC information in example 8
XX SQ Sequence 1356 AA;
Query Match 85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKDIVLPI 11

```



```
Db      1171 DGKDYIVLPI 1180
|||||
AAU79429 standard; protein; 1356 AA.
AC      AAU79429;
XX
XX
XX      02-JUL-2002 (first entry)
DE      Human Kinase insert domain-containing receptor mutant Y1214F.
XX
XX      Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
KW      fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic; mutin;
KW      antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW      angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
XX      Homo sapiens.
OS
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      Misc-difference 1214
FT      /note= "Wild-type Tyr substituted by Phe"
XX
XX      WO200229090-A1.
PN
XX
XX      11-APR-2002.
PD
XX
XX      02-OCT-2001; 2001WO-JP008684.
PF
XX
XX      03-OCT-2000; 2000JP-00303694.
PR
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
PA      (SHIB/) SHIBUYA M.
XX
XX      Shibuya M, Takahashi T, Furuya A, Shitara K;
PI
XX
XX      WPI; 2002-352237/38.
DR
XX
XX      Screening substances inhibiting the binding of signal-transducing
PT      molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT      cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT      of e.g. tumor.
XX
XX      Example 8; Page; 81pp; Japanese.
XX
XX      The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX      (kinase insert domain-containing receptor/fetal liver kinase-1) is by
XX      using a substance inhibiting the binding of a signal-transducing molecule
XX      to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
XX      included are methods of detecting/inhibiting/screening for cell
XX      proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
XX      phosphorylation at tyrosine at the 1175-position using the binding
XX      inhibitors, compounds obtained by the screening methods, drugs containing
XX      the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-1
XX      -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
XX      monoclonal antibody or its fragment, a recombinant vector containing the
XX      DNA and a transformant obtained by transferring the recombinant vector
XX      into a host cell. The method is useful for screening substances
XX      inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
XX      phosphorylated at tyrosine at 1175-position, as cell proliferation
XX      inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
XX      diabetic omentopathy and chronic rheumatoid arthritis. A method for
XX      detecting angiogenesis is also provided. The present sequence is the
XX      Human KDR/FLK-1 mutant where Tyr at 1214 is replaced by Phe. Note: The
XX      present sequence is not shown in the specification but was created by the
XX      indexer using the KDR/FLK-1 sequence appearing as AAU7926 and the
XX      information in example 8
XX      Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
|||||
DB      1171 DGKDYIVLPI 1180
XX
XX
XX      RESULT 15
AAU79426
ID      AAU79426 standard; protein; 1356 AA.
XX
XX      AC      AAU79426;
XX
XX      DT      02-JUL-2002 (first entry)
XX
XX      DE      Human Kinase insert domain-containing receptor.
XX
XX      Human; KDR; kinase insert domain-containing; receptor; FLK-1;
KW      fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic;
KW      antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW      angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
XX      Homo sapiens.
OS
OS      WO200229090-A1.
PN
XX
XX      11-APR-2002.
PD
XX
XX      02-OCT-2001; 2001WO-JP008684.
PF
XX
XX      03-OCT-2000; 2000JP-00303694.
PR
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
PA      (SHIB/) SHIBUYA M.
XX
XX      Shibuya M, Takahashi T, Furuya A, Shitara K;
PI
XX
XX      WPI; 2002-352237/38.
DR
XX
XX      Screening substances inhibiting the binding of signal-transducing
PT      molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT      cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT      of e.g. tumor.
XX
XX      Disclosure; Page 65-71; 81pp; Japanese.
XX
XX      The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX      (kinase insert domain-containing receptor/fetal liver kinase-1) is by
XX      using a substance inhibiting the binding of a signal-transducing molecule
XX      to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
XX      included are methods of detecting/inhibiting/screening for cell
XX      proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
XX      phosphorylation at tyrosine at the 1175-position using the binding
XX      inhibitors, compounds obtained by the screening methods, drugs containing
XX      the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-1
XX      -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
XX      monoclonal antibody or its fragment, a recombinant vector containing the
XX      DNA and a transformant obtained by transferring the recombinant vector
XX      into a host cell. The method is useful for screening substances
XX      inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
XX      phosphorylated at tyrosine at 1175-position, as cell proliferation
XX      inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
XX      diabetic omentopathy and chronic rheumatoid arthritis. A method for
XX      detecting angiogenesis is also provided. The present sequence is the
XX      Human KDR/FLK-1 protein
XX
XX      Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 DGKDYIVLPI 11
| | | | | | | |
Db 1171 DGKDYIVLPI 1180

Search completed: December 9, 2005, 10:28:47
Job time : 60.4906 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:20:05 ; Search time 60.8113 Seconds
(without alignments)
127.621 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	85.5	180	Q8MI23 SHEEP	Q8mi23 ovis aries
2	53	85.5	207	Q9N112 SHEEP	Q9n112 ovis aries
3	53	85.5	1356	1 VGR22 HUMAN	P35968 homo sapien
4	53	85.5	1451	2 Q59EB0 HUMAN	Q8c600 homo sapien
5	50	80.6	341	2 Q8CD05 MOUSE	Q8cd05 mus musculus
6	50	80.6	1343	1 VGR22 RAT	Q80775 rattus norv
7	50	80.6	1343	2 Q5PQU0 RAT	Q5pq00 rattus norv
8	50	80.6	1345	2 Q8VCD0 MOUSE	Q8vcd0 mus musculus
9	50	80.6	1348	1 VGR22 COTJA	P52583 coturnix co
10	50	80.6	1348	2 Q677M1 CHICK	Q677m1 gallus gall
11	50	80.6	1367	1 VGR22 MOUSE	P35918 mus musculus
12	47	75.8	181	2 Q709P9 HUMAN	Q709p9 homo sapien
13	47	75.8	181	2 Q709Q0 HUMAN	Q709q0 homo sapien
14	47	75.8	181	2 Q8WLT2 HUMAN	Q8wlt2 homo sapien
15	47	75.8	181	2 Q4GX99 HUMAN	Q4gx99 homo sapien
16	47	75.8	273	2 Q8SNC8 HUMAN	Q8snc8 homo sapien
17	47	75.8	304	2 Q8SNC1 HUMAN	Q8snc1 homo sapien
18	47	75.8	445	2 Q7VOC6 PROMP	Q7voc6 prochloroco
19	46	74.2	415	2 Q4HSF2 CAMUP	Q4hsf2 campylobact
20	46	74.2	416	2 Q4HIW6 CAMLA	Q4hiw6 campylobact
21	45	72.6	416	1 PUR2 CAMJE	Q9pm47 campylobact
22	45	72.6	416	1 PUR2 CAMJR	Q5ht11 campylobact
23	45	72.6	416	2 Q4HH59 CAMCO	Q4hh59 campylobact
24	44	71.0	178	2 Q9XS54 RABIT	Q9xs54 coryctolagus
25	44	71.0	217	2 Q4UJ21 THEAN	Q4uj21 theileria a
26	44	71.0	369	2 Q5NTF8 9BACT	Q5ntf8 uncultured
27	44	71.0	431	2 Q7MUW7 FORGI	Q7muw7 porphyromon
28	43	69.4	150	2 Q6M9V0 PARUM	Q6m9v0 parachlamyd
29	43	69.4	419	2 Q7M9I6 WOLSU	Q7m9i6 wolnella s
30	42	67.7	177	2 Q7YXP4 AOTVO	Q7ypx4 aotus vocif
31	42	67.7	177	2 Q7YXP5 AOTVO	Q7ypx5 aotus vocif

32 42 67.7 177 2 Q7YXP6 AOTVO Q7ypx6 aotus vocif
33 42 67.7 177 2 Q7YYP2 AOTNI Q7ypy2 aotus nigri
34 42 67.7 177 2 Q7YYP5 AOTNI Q7ypy5 aotus nigri
35 42 67.7 177 2 Q7YYP7 AOTNA Q7ypy7 aotus nancy
36 42 67.7 225 2 Q5GGV8 MACNE Q5ggv8 macaca neme
37 42 67.7 351 2 Q70PL5 MACMU Q70pl5 macaca mula
38 42 67.7 351 2 Q70PL6 MACMU Q70pl6 macaca mula
39 42 67.7 354 2 Q5QGW4 MACNE Q5qgw4 macaca neme
40 42 67.7 355 2 Q5DLS0 AOTNA Q5dlso aotus nancy
41 42 67.7 357 2 Q5DLR6 AOTNA Q5dlr6 aotus nancy
42 42 67.7 357 2 Q5DLR9 AOTNA Q5dlr9 aotus nancy
43 42 67.7 357 2 Q5DLS1 AOTNA Q5dls1 aotus nancy
44 42 67.7 357 2 Q5DLT2 AOTVO Q5dlt2 aotus vocif
45 42 67.7 362 2 Q4W7D8 MACFA Q4w7d8 macaca fasc

ALIGNMENTS

RESULT 1
Q8MI23 SHEEP
ID Q8MI23_SHEEP PRELIMINARY; PRT; 180 AA.
AC Q8MI23;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor receptor-2 (Fragment).
OS Ovis aries (Sheep). Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placental artery endothelium;
RA Chung J.-Y., Tsou S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534634; AAN04105.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8MI23; 1-150.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT Receptor.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 20599 MW; 70B5F444574779A0 CRC64;

Query Match 85.5%; Score 53; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 2 DGKDYIVLPI 11
|||||||
DB 153 DGKDYIVLPI 162

RESULT 2
Q9N112 SHEEP
ID Q9N112_SHEEP PRELIMINARY; PRT; 207 AA.
AC Q9N112;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

```

DE KDR/flk-1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Scholz T.D., Segar J.L.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233076; AAF60280.1; -, mRNA.
DR HSP; P35968; 1VR2.
DR SMR; Q9N12; 1-157.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
FT NON_TER 207
FT NON_TER 207
SQ SEQUENCE 207 AA; 23691 MW; 51C3950D82F988F6 CRC64;

Query Match 85.5%; Score 53; DB 2; Length 207;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 160 DGKDYIVLPI 169

RESULT 3
VGFPR2 HUMAN STANDARD; PRT; 1356 AA.
ID VGFPR2_HUMAN STANDARD; PRT; 1356 AA.
AC P35968; O60723; Q14178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Kinase insert domain receptor) (protein-tyrosine kinase
DE receptor Flk-1).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yin L.Y., Wu Y., Patterson C.;
RL "Full length human KDR/flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUS=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor KDR (VEGFR-2)";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 3-1356.
RC TISSUS=Umbilical vein;
RX MEDLINE=92019839; PubMed=1656371;
RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,
RA Shows T.B.;

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RT "Identification of a new endothelial cell growth factor receptor
RT tyrosine kinase.";
RL Oncogene 6:1677-1683(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-22.
RA MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION
RX MEDLINE=93038639; PubMed=1417831;
RA Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
RA Armellino D.C., Gospodarowicz D., Boehlen P.;
RT "Identification of the KDR tyrosine kinase as a receptor for vascular
RT endothelial cell growth factor.";
RL Biochem. Biophys. Res. Commun. 187:1579-1586(1992).
CC -!- FUNCTION: Receptor for VEGF or VEGFR. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF035121; AAB88005.1; -, mRNA.
DR EMBL; AF063658; AAC16450.1; -, mRNA.
DR EMBL; X61656; CAA43837.1; -, mRNA.
DR EMBL; L04947; AAA59459.1; -, mRNA.
DR EMBL; X89776; CAA61916.1; -, Genomic_DNA.
DR PIR; JCI402; JCI402.
DR PDB; 1VR2; X-ray; A=806-1171.
DR Ensembl; ENSG00000128052; Homo sapiens.
DR HGNC; HGNC:6307; KDR.
DR MIM; 191306; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR01832; VEGFRECEPTR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR PRODOM; PD000001; Prot_kinase; 2.
DR SMART; SM00408; Igc2; 2.
DR SMART; SM00219; Tyrkc; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR 3D-structure; Angiogenesis; ATP-binding; Developmental protein;
DR Differentiation; Glycoprotein; Immunoglobulin domain; Kinase;
DR Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Repeat;
DR Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
DR SIGNAL 1 19 Potential.

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FT CHAIN 20 1356 Vascular endothelial growth factor
FT receptor 2.
FT Extracellular (Potential).
FT Transmem 765 789 Potential.
FT TOPO_DOM 790 1356 Cytoplasmic (Potential).
FT DOMAIN 46 110 Ig-like C2-type 1.
FT DOMAIN 141 207 Ig-like C2-type 2.
FT DOMAIN 224 320 Ig-like C2-type 3.
FT DOMAIN 328 414 Ig-like C2-type 4.
FT DOMAIN 421 548 Ig-like C2-type 5.
FT DOMAIN 551 660 Ig-like C2-type 6.
FT DOMAIN 667 753 Ig-like C2-type 7.
FT DOMAIN 834 1162 Protein kinase.
FT NP_BIND 1028 848 ATP (By similarity).
FT BINDING 868 888 ATP (By similarity).
FT MOD_RES 1059 1059 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 318 318 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 395 395 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 523 523 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 580 580 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 613 613 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 619 619 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 631 631 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 675 675 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 704 704 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 721 721 N-linked (GlcNAc...) (Potential).
FT VARIANT 297 297 V -> I (in dbSNP:2305948).
FT VARIANT 472 472 /FTID=VAR_022071.
FT VARIANT 472 472 Q -> H (in dbSNP:1870377).
FT CONFLICT 2 2 /FTID=VAR_020353.
FT CONFLICT 772 772 A -> T (in Ref. 3).
FT CONFLICT 787 787 R -> G (in Ref. 3).
FT CONFLICT 835 835 K -> N (in Ref. 3).
FT CONFLICT 848 848 V -> E (in Ref. 3).
FT CONFLICT 1347 1347 S -> T (in Ref. 3).
FT CONFLICT 1356 1356 S -> T (in Ref. 3).
FT SEQUENCE 1356 AA; 151527 MW; 59E7C44B05CEBEB3 CRC64;

Query Match 85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1171 DGKDYIVLPI 1180

RESULT 4
Q59EB0 HUMAN PRELIMINARY; PRT; 1451 AA.
ID Q59EB0;
AC Q59EB0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kinase insert domain receptor (A type III receptor tyrosine kinase)
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209901; BAD93138.1; -, mRNA.
KW Kinase; Receptor.
FT NON_TER 1
FT SEQUENCE 1451 AA; 161601 MW; 915FE64B51EFAOCB CRC64;

Query Match 85.5%; Score 53; DB 2; Length 1451;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1266 DGKDYIVLPI 1275

RESULT 5
Q8CD05 MOUSE PRELIMINARY; PRT; 341 AA.
ID Q8CD05;
AC Q8CD05;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 14 days embryo thymus cDNA, RIKEN full-length enriched
DE library, clone:6130401C07 product:kinase insert domain protein
DE receptor, full insert sequence. (Fragment).
DE Name=Kdr;
GN Mus musculus (Mouse).
OS Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

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RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RN prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RN sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031739; BAC27532.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8CD05; 1-162.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR GO; GO:0030097; P:hemoiesis; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase; Receptor.
FT NON_TER
SQ SEQUENCE 341 AA; 38302 MW; E2B4DCC4BB481195 CRC64;
Query Match 80.6%; Score 50; DB 2; Length 341;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKQYIVLPI 11
Db 165 DGKQYIVLPI 174
RESULT 6
VGFR2_RAT

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ID VGFR2_RAT STANDARD; PRT; 1343 AA.
AC Q08775;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1).
GN Name=Kdr; Synonyms=Flk1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -1- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U93306; AAB97508.1; -; mRNA.
DR EMBL; U93307; AAB97509.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR RGD; 2965; Kdr.
DR GO; GO:0019838; F:growth factor binding; IMP.
DR GO; GO:0005021; P:vascular endothelial growth factor receptor. ; IMP.
DR GO; GO:0048010; P:vascular endothelial growth factor receptor. ; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinasII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1343 Vascular endothelial growth factor
FT receptor 2.
FT TOPO_DOM 20 760 Extracellular (Potential).
FT TRANSMEM 761 782 Potential.
FT TOPO_DOM 783 1343 Cytoplasmic (Potential).

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FT DOMAIN 46 109 Ig-like C2-type 1.
FT DOMAIN 141 207 Ig-like C2-type 2.
FT DOMAIN 224 320 Ig-like C2-type 3.
FT DOMAIN 328 414 Ig-like C2-type 4.
FT DOMAIN 421 540 Ig-like C2-type 5.
FT DOMAIN 547 654 Ig-like C2-type 6.
FT DOMAIN 663 749 Ig-like C2-type 7.
FT DOMAIN 830 1158 Protein kinase.
FT NP_BIND 836 844 ATP (By similarity).
FT ACT_SITE 1024 1024 By similarity.
FT BINDING 864 864 ATP (By similarity).
FT MOD_RES 1055 1055 Phosphotyrosine (by autocatalysis) (By similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 318 318 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 395 395 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 576 576 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 615 615 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 627 627 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 671 671 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 700 700 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 717 717 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1343 AA; 150394 MW; AD7E509B62D3FF4 CRC64;

Query Match 80.6%; Score 50; DB 1; Length 1343;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1167 DGKDYIVLPM 1176
|||||||
1167 DGKDYIVLPM 1176

RESULT 7
QSPQUO RAT
ID Q5POU0 RAT PRELIMINARY; PRT; 1343 AA.
AC Q5POU0_
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Kdr protein.
GN Name=Kdr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Director MGC Project;
RL Submitted (DSC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087029; AAH87029.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007159; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; Recepttyr_kinsIII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PR01832; VEGFRRECEPTOR.
DR PRINTS; PR01834; VEGFRRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 7.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ SEQUENCE 1343 AA; 150274 MW; F4B906E8012A5C59 CRC64;

Query Match 80.6%; Score 50; DB 2; Length 1343;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1167 DGKDYIVLPM 1176
|||||||
1167 DGKDYIVLPM 1176

RESULT 8
Q8VCD0 MOUSE
ID Q8VCD0 MOUSE PRELIMINARY; PRT; 1345 AA.
AC Q8VCD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinase insert domain protein receptor.
GN Name=Kdr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020530; AAH20530.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG0000062960; Mus musculus.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrknsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTOR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1345 AA; 150460 MW; 11859F8A58A33A39 CRC64;

Query Match 80.6%; Score 50; DB 2; Length 1345;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKQIVLPLI 11
DQ 1169 DGKQIVLPLM 1178

RESULT 9
VGF2_COTJA STANDARD; PRT; 1348 AA.
AC P52583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Endothelial kinase receptor EK1) (Quek 1) (Quek1).
GN Name=KDR; Synonyms=EK1, FLK-1;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=97017121; PubMed=8863722; DOI=10.1016/0378-1119(96)00159-X;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Molecular cloning of Quek 1 and 2, two quail vascular endothelial
RT growth factor (VEGF) receptor-like molecules.";
RL Gene 174:3-8(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 910-1348.
RC TISSUE=Spinal cord;
RX MEDLINE=93378866; PubMed=8396413; DOI=10.1016/0925-4773(93)90096-G;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Two molecules related to the VEGF receptor are expressed in early
RT endothelial cells during avian embryonic development.";
RL Mech. Dev. 42:33-48(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 764-880, AND CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909; DOI=10.1006/dbio.1995.1180;
RA Flamme I., Breiter G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1)
RT are expressed during vasculogenesis and vascular differentiation in
RT the quail embryo.";
RL Dev. Biol. 169:699-712(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1023-1079.
RX PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo.";
CC Oncogene 7:2479-2487(1992).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In all endothelial tissues during onset of
CC vascularization. In later development, present in lung, heart,
CC intestine and skin.
CC -!- DEVELOPMENTAL STAGE: Expressed in whole mesoderm at onset of
CC gastrulation. From day 2, confined to endothelial tissues and
CC expression continues to be widespread throughout vascularization
CC until E9 where it becomes restricted to specific regions such as
CC the spinal chord and heart valves.
CC -!- INDUCTION: In vitro, it is induced by basic fibroblast growth
CC factor (bFGF), uniquely in the first 24 hours of cell culture.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X83288; CAA58268.1; -; mRNA.
CC EMBL; S65205; AAB28127.1; -; mRNA.
CC EMBL; S78345; AAB34594.1; -; mRNA.
CC PIR; JC4953; S51656.
CC HSSP; P35968; 1VR2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001824; RecepttyrknsIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR008266; Tyr_pkinase_AS.


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DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGPRECEPTOR.
DR PRINTS; PR01834; VEGPRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 20
FT CHAIN 21 1348
FT TOPO_DOM 21 756
FT TRANSMEM 757 777
FT TOPO_DOM 778 1348
FT DOMAIN 43 106
FT DOMAIN 138 202
FT DOMAIN 220 312
FT DOMAIN 320 405
FT DOMAIN 412 534
FT DOMAIN 540 651
FT DOMAIN 658 744
FT DOMAIN 825 1155
FT NP_BIND 831 839
FT ACT_SITE 1021 1021
FT BINDING 859 859
FT CARBOHYD 43 43
FT CARBOHYD 47 47
FT CARBOHYD 63 63
FT CARBOHYD 93 93
FT CARBOHYD 138 138
FT CARBOHYD 153 153
FT CARBOHYD 201 201
FT CARBOHYD 240 240
FT CARBOHYD 290 290
FT CARBOHYD 310 310
FT CARBOHYD 365 365
FT CARBOHYD 386 386
FT CARBOHYD 513 513
FT CARBOHYD 556 556
FT CARBOHYD 603 603
FT CARBOHYD 613 613
FT CARBOHYD 622 622
FT CARBOHYD 666 666
FT CARBOHYD 688 688
FT CARBOHYD 710 710
FT CONFLICT 865 865
FT SEQUENCE 1348 AA; 150306 MW; A5E419A76FD5FB3 CRC64;

Query Match 80.6%; Score 50; DB 1; Length 1348;
Best Local Similarity 80.0%; Pred. No. 5.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1164 DGKDYVVLPL 1173

RESULT 10
Q677M1.CHICK PRELIMINARY; PRT; 1348 AA.
AC Q677M1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
```

```
DE Vascular endothelial growth factor receptor 2.
GN Name=Flk1;
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Hashimoto T.;
RT "Modulation of retinal neurogenesis by vascular endothelial growth
factor.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RT EMBL; AY382882; AAR26285.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Ser_thr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGPRECEPTOR.
DR PRINTS; PR01834; VEGPRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 5.
DR SMART; SM00408; IGC2; 7.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Receptor.
SQ SEQUENCE 1348 AA; 150121 MW; F6E0F021CA839D65 CRC64;

Query Match 80.6%; Score 50; DB 2; Length 1348;
Best Local Similarity 80.0%; Pred. No. 5.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1164 DGKDYVVLPL 1173

RESULT 11
VGFR2_MOUSE
ID VGFR2_MOUSE STANDARD; PRT; 1367 AA.
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (BC 2.7.1.112)
DE (VEGFR-2) (protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (Kinase NYK).
GN Name=Kdr; Synonyms=Flk-1, Flk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
```

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Embryo;
RX MEDLINE=9320880; PubMed=7681362; DOI=10.1016/0092-8674(93)90573-9;
RA Millauer B., Witzmann-Voss S., Schurich H., Martinez R.,
RA Mueller N.P.H., Risau W., Ullrich A.;
RT "High affinity VEGF binding and developmental expression suggest Flk-1
RT as a major regulator of vasculogenesis and angiogenesis.";
RL Cell 72:835-846(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/He; TISSUE=Fetal liver;
RX MEDLINE=92020984; PubMed=1717995;
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
RA Lemischka I.R.;
RT "A receptor tyrosine kinase cDNA isolated from a population of
RT enriched primitive hematopoietic cells and exhibiting close genetic
RT linkage to c-kit.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93141255; PubMed=8423388;
RA Oelrichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.;
RT "NYK/FUK-1: a putative receptor protein tyrosine kinase isolated from
RT E10 embryonic neuroepithelium is expressed in endothelial cells of the
RT developing embryo.";
RL Oncogene 8:11-18(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-15.
RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93361481; PubMed=8356051;
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;
RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth
RT factor and is selectively expressed in vascular endothelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung,
CC kidney, brain and skeletal muscle, but is also expressed at lower
CC levels in most other adult tissues.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X70842; CAA50192.1; -; mRNA.
CC EMBL; X59397; CAA42040.1; -; mRNA.
CC EMBL; S53103; AAB25043.1; -; mRNA.
CC EMBL; X89777; CAA61917.1; -; Genomic_DNA.
CC PIR; A41228; A41228.
CC HSP; P15968; 1VR2.
CC Ensembl; ENSMUSG00000062960; Mus musculus.
CC MGI; MGI:96683; Kdr.

DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR GO; GO:0030097; P:hemopoiesis; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferrase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1367 Vascular endothelial growth factor
FT receptor 2.
FT Extracellular (Potential).
FT POTENTIAL.
FT TOPO_DOM 20 762 Cytoplasmic (Potential).
FT TRANSMEM 763 784
FT TOPO_DOM 785 1367
FT DOMAIN 46 111 Ig-like C2-type 1.
FT DOMAIN 143 209 Ig-like C2-type 2.
FT DOMAIN 226 325 Ig-like C2-type 3.
FT DOMAIN 330 416 Ig-like C2-type 4.
FT DOMAIN 423 542 Ig-like C2-type 5.
FT DOMAIN 549 656 Ig-like C2-type 6.
FT DOMAIN 665 751 Ig-like C2-type 7.
FT DOMAIN 832 1160 protein kinase.
FT NP_BIND 838 846 ATP (By similarity).
FT ACT_SITE 1026 1026 By similarity.
FT BINDING 866 866 ATP (By similarity).
FT MOD_RES 1057 1057 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 247 247 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 320 320 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 397 397 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 521 521 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 617 617 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 629 629 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 673 673 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 702 702 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 719 719 N-linked (GlcNAc...) (Potential).
FT CONFLICT 25 25 P -> T (in Ref. 1).
FT CONFLICT 679 679 G -> D (in Ref. 3).
FT CONFLICT 783 784 LV -> VL (in Ref. 1).
FT CONFLICT 917 917 S -> C (in Ref. 1).
FT CONFLICT 1341 1367 QLTSLGSGVGPAPPPTPGNHERGAA -> RSPPV (in
Ref. 3).
SQ SEQUENCE 1367 AA; 152517 MW; EFC99704F1DCA266 CRC64;

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Query Match      80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. No. 5.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKGKDYIVLP 11
DB 1169 DKGKDYIVLPM 1178

RESULT 12
Q709P9 HUMAN
ID Q709P9 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q709P9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral blood;
RA Darke C., Hammond L., Street J., Downing J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606948; CAE54963.1; -; Genomic_DNA.
DR HSSP; P30474; IALN.
DR SMR; Q709P9; 1-181.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 181
FT NON_TER 181
SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
DB 117 CDGKDYIAL 125

RESULT 13
Q709Q0 HUMAN
ID Q709Q0 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q709Q0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral blood;
RA Darke C., Hammond L., Street J., Downing J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606947; CAE54962.1; -; Genomic_DNA.
DR HSSP; P30474; IALN.
DR SMR; Q709Q0; 1-181.

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
DB 117 CDGKDYIAL 125

RESULT 14
Q8WLT2 HUMAN
ID Q8WLT2 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q8WLT2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bennett T.T., Cavett J.W., Sidebottom D.A., Bardet W., Pruett B.N.,
RA Orina J., Luis A.D., Hildebrand W.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY045736; AAL10679.1; -; Genomic_DNA.
DR EMBL; AY045735; AAL10679.1; JOINED; Genomic_DNA.
DR HSSP; P30474; IALN.
DR SMR; Q8WLT2; 1-181.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 181
FT NON_TER 181
SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
DB 117 CDGKDYIAL 125

RESULT 15
Q4GX9 HUMAN
ID Q4GX9 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q4GX9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE HLA Class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=41241; TISSUE=Peripheral blood;
 RA Hammond L., Street J., Darke C.;
 RT "Confirmatory sequence and serology of HLA-B*3541.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AM040977; CAJ13856.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match 75.8%; Score 47; DB 2; Length 181;
 Best Local Similarity 88.9%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDGKDYIVL 9
 Db 117 CDGKDYIAL 125

Search completed: December 9, 2005, 10:33:45
 Job time : 62.8113 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:21:00 ; Search time 9.54717 Seconds
(without alignments)
110.858 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	85.5	1356	JC1402	protein-tyrosine k
2	50	80.6	1348	S51656	vascular endotheli
3	50	80.6	1367	A41228	protein-tyrosine k
4	45	72.6	416	D81332	phosphoribosylamin
5	41.5	66.9	662	T44219	hypothetical prote
6	41.5	66.9	662	T44034	hypothetical prote
7	40	64.5	108	C72231	ATP synthase Fl, s
8	40	64.5	984	H90029	hypothetical prote
9	39	62.9	598	F83977	hypothetical prote
10	39	62.9	633	T23090	hypothetical prote
11	39	62.9	953	D82068	valyl-tRNA synthet
12	38.5	62.1	788	I59282	diacylglycerol kin
13	38	61.3	84	S51100	hypothetical prote
14	38	61.3	89	I72029	MHC HLA-A3-alpha-2
15	38	61.3	89	I56009	MHC HLA-A2-alpha-2
16	38	61.3	137	I80172	class I histocompa
17	38	61.3	137	I80175	class I histocompa
18	38	61.3	137	I80173	class I histocompa
19	38	61.3	137	I80176	class I histocompa
20	38	61.3	137	I80174	class I histocompa
21	38	61.3	137	I38875	MHC class I antige
22	38	61.3	137	I38860	MHC class I antige
23	38	61.3	137	I38874	MHC class I antige
24	38	61.3	137	I38876	MHC class I antige
25	38	61.3	181	I79640	MHC cell surface a
26	38	61.3	181	I59188	MHC cell surface g
27	38	61.3	182	A49411	human leukocyte an
28	38	61.3	206	I37529	HLA-Cw7 - human (f
29	38	61.3	206	I37528	HLA-Cw1 - human (f

ALIGNMENTS

RESULT 1

JC1402
protein-tyrosine kinase (BC 2.7.1.112) KDR - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 05-Oct-2004
C:Accession: JC1402; I58357
R;Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gosi
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A:Title: Identification of the KDR tyrosine kinase as a receptor for vascular endotheli.
A:Reference number: JC1402; MUID:93038639; PMID:1417831
A:Accession: JC1402
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-616, 'E', 618-700, 'E', 702-748, 'F', 750-1263, 'I', 1265-1290, 'P', 1292
A:Cross-references: UNIPROT:P35968; UNIPARC:UPI000017A3C3; EMBL:X61656; NID:G31717
R;Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.
Oncogene 6, 1677-1683, 1991
A:Title: Identification of a new endothelial cell growth factor receptor tyrosine kinas
A:Reference number: I58357; MUID:92019839; PMID:1656371
A:Accession: I58357
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 3-1356 <TER2>
A:Cross-references: UNIPARC:UPI000016A991; GB:I04947; NID:G186674; PIDN:AAAS9459.1; PID
C:Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.

C:Genetics:
A:Gene: GDB:KDR
A:Cross-references: GDB:127921; OMIM:191306
A:Map position: 4q12-4q12
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
F;766-790/Domain: transmembrane #status predicted <FMW>
F;832-1167/Domain: protein kinase homology <KIN>
F;840-848/Region: protein kinase ATP-binding motif

Query Match 85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

Db 1171 DGKDYIVLPI 1180

RESULT 2

S51656
vascular endothelial growth factor receptor 1 precursor - Japanese quail
N;Alternate names: quail endothelial kinase 1 (Quek 1); vascular endothelial growth fac
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
C:Accession: JCA4953; A56598; I51162; S51656
R;Richmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996

A>Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A:Reference number: JC4953; MUID:97017121; PMID:8863722
A:Accession: JC4953
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1348 <EIC1>
A:Cross-references: UNIPROT:P52583; UNIPARC:UPI0000138775; EMBL:X83288; NID:G603523; PID:
A:Note: submitted to the EMBL Data Library, December 1994
R:Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Mach. Dev. 42, 33-48, 1993
A>Title: Two molecules related to the VEGF receptor are expressed in early endothelial c
A:Reference number: A56598; MUID:93378866; PMID:8396413
A:Contents: E16 spinal cord
A:Accession: A56598
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 910-1348 <EIC2>
A:Cross-references: UNIPARC:UPI0000171474; GB:S65205; NID:G410680; PIDN:AAB28127.1; PID:
A:Note: sequence extracted from NCBI backbone (NCBIN:137162, NCBI:P:137163)
R:Marcelle, C.; Eichmann, A.
Oncogene 7, 2479-2487, 1992
A>Title: Molecular cloning of a family of protein kinase genes expressed in the avian en
A:Reference number: I50595; MUID:93096482; PMID:1281306
A:Accession: I51162
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1023-1079 <MAR>
A:Cross-references: UNIPARC:UPI00000F94F0; EMBL:X69694; NID:G935226; PIDN:CAA49364.1; PI
A:Note: the species is not identified by the authors; the most probable species is shown
C:Comment: This protein is an endothelial-specific receptor and binds vascular endotheli
C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1348/Product: vascular endothelial growth factor receptor 1 #status predicted <MAT>
F:756-777/Domain: transmembrane #status predicted <TM>
F:823-1160/Domain: protein kinase homology <KIN>
F:831-839/Region: protein kinase ATP-binding motif

Query Match 80.6%; Score 50; DB 2; Length 1348;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
|||||:
Db 1164 DGKDYVVLPL 1173

RESULT 3
A41228
protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C:Species: Mus musculus (house mouse)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
C:Accession: A41228; A46065; I58365; I58832; S29991
R:Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A>Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitiv
A:Reference number: A41228; MUID:92020984; PMID:1717995
A:Accession: A41228
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1367 <MAT>
A:Cross-references: UNIPROT:P35918; UNIPARC:UPI0000028D93; GB:X59397; NID:G50976; PIDN:C
R:Millauer, B.; Wozniak-Voos, S.; Schuruch, H.; Martinez, R.; Mollner, N.P.; Risau, W.;
Cell 72, 835-846, 1993
A>Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a maj
A:Reference number: A46065; MUID:93208880; PMID:7681362
A:Accession: A46065
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-24,'T',26-782,'VL',785-916,'C',918-1367 <MIL>
A:Cross-references: UNIPARC:UPI000003CA97; GB:X70842; NID:G57923; PIDN:CAA50192.1; PID:G
A:Note: submitted to the EMBL Data Library, January 1993
A:Note: sequence extracted from NCBI backbone (NCBI:P:128064)
R:Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemiecki, A.; Wilks, A.F.

Oncogene 8, 11-18, 1993
A>Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embryo
A:Reference number: I58365; MUID:93141255; PMID:8423988
A:Accession: I58365
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-678,'D',680-1340,'R3PPV' <OEL>
A:Cross-references: UNIPARC:UPI0000170C47; GB:S53103; NID:G264004; PIDN:AAB25043.1; PID:
C:Genetics:
A:Gene: FLK-1; NYK
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F:830-1165/Domain: protein kinase homology <KIN>
F:838-846/Region: protein kinase ATP-binding motif

Query Match 80.6%; Score 50; DB 2; Length 1367;
Best Local Similarity 90.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
|||||:
Db 1169 DGKDYIVLPM 1178

RESULT 4
D81332
phosphoribosylamine-glycine ligase (EC 6.3.4.13) Cj1250 [imported] - Campylobacter jejuni
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81332
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: D81332
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-416 <PAR>
A:Cross-references: UNIPROT:Q9PN47; UNIPARC:UPI0000132A1B; GB:AL139077; GB:AL111168; NID
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: purD; Cj1250
C:Superfamily: phosphoribosylamine-glycine ligase; phosphoribosylamine-glycine ligase ho
C:Keywords: ligase

Query Match 72.6%; Score 45; DB 2; Length 416;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLP 10
|||||:
Db 197 CDGNDFVLLP 206

RESULT 5
T44219
hypothetical protein U74 [imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
C:Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44219
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A>Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: Z22734; MUID:99412318; PMID:10482553
A:Accession: T44219
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-662 <DOM>
A:Cross-references: UNIPROT:P52451; UNIPARC:UPI000012C60D; EMBL:AF157706; PIDN:AAB06357.
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Note: U74

Query Match 66.9%; Score 41.5; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 CDGKD-YIVLPI 11
Db 462 CDGKDSHVWVPL 473
||||| :|:|:
| | | | | :|:|:
| | | | | :|:|:
| | | | | :|:|:

RESULT 6
T44034
hypothetical protein U74 [imported] - human herpesvirus 6 (strain HST)
C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
R:Accession: T44034
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732; MUID:99412319; PMID:10482554
A:Accession: T44034
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-662 <ISE>
A:Cross-references: UNIPROT:Q9WT01; UNIPARC:UPI00000FOBBB; EMBL:AB021506; NID:G4995977;
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U74

Query Match 66.9%; Score 41.5; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 CDGKD-YIVLPI 11
Db 462 CDGKDSHVWVPL 473
||||| :|:|:
| | | | | :|:|:
| | | | | :|:|:
| | | | | :|:|:

RESULT 7
C72231
ATP synthase F1, subunit epsilon - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72231
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <ARN>
A:Cross-references: UNIPROT:Q9X1U5; UNIPARC:UPI0000126520; GB:AE001805; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1609

Query Match 64.5%; Score 40; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
Db 67 CDGKDVIII 75
||||| :|:|:
| | | | | :|:|:
| | | | | :|:|:
| | | | | :|:|:

RESULT 8
H90029
hypothetical protein SA2102 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004
C:Accession: H90029
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-984 <KUR>
A:Cross-references: UNIPROT:Q99RW4; UNIPARC:UPI00000D776F; GB:BA000018; PID:gl3702109; I
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2102
C:Superfamily: NAD-dependent formate dehydrogenase, alpha subunit

Query Match 64.5%; Score 40; DB 2; Length 984;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 10
Db 10 DGKDYIVLP 18
||||| :|:|:
| | | | | :|:|:
| | | | | :|:|:
| | | | | :|:|:

RESULT 9
R83977
hypothetical protein BH2622 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: R83977
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: R83977
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-598 <STO>
A:Cross-references: UNIPROT:Q9KM3; UNIPARC:UPI00000C3F65; GB:AP001516; GB:BA000004; NI
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2622
C:Superfamily: *Escherichia coli* plasmid ColV-K30 aerobactin biosynthesis protein iuca

Query Match 62.9%; Score 39; DB 2; Length 598;
Best Local Similarity 45.5%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDGKDYIVLPI 11
Db 230 COADDYVLLPV 240
||||| :|:|:
| | | | | :|:|:
| | | | | :|:|:
| | | | | :|:|:

RESULT 10
T23090
hypothetical protein H13N06.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23090
R:Lennard, N.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19673
A:Accession: T23090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-633 <WIL>
A:Cross-references: UNIPROT:Q9XTQ6; UNIPARC:UPI000017BA61; EMBL:Z99942; PIDN:CAB17071.1
A:Experimental source: clone H13N06
C:Genetics:
A:Gene: CBSP:H13N06.6

A;Map position: X
A;Introns: 134/3; 179/3; 206/3; 381/2; 420/3; 541/2

Query Match 62.9%; Score 39; DB 2; Length 633;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLP 10
||:||||
Db 171 CDSRDYAFLP 180

RESULT 11

E82068
valyl-tRNA synthetase VC2503 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82068
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82068
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-953 <HEI>
A;Cross-references: UNIPROT:Q9KPF73; UNIPARC:UPI000013670E; GB:AE004320; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2503
A;Map position: 1
C;Superfamily: valine-tRNA ligase

Query Match 62.9%; Score 39; DB 2; Length 953;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 212 DGKDYIVV 219

RESULT 12

I59282
diacylglycerol kinase (EC 2.7.1.107) gamma - rat
C;Species: Rattus sp. (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I59282
R;Goto, K.; Funayama, M.; Kondo, H.
Proc. Natl. Acad. Sci. U.S.A. 91, 13042-13046, 1994
A;Title: Cloning and expression of a cytoskeleton-associated diacylglycerol kinase that
A;Reference number: I59282; MUID:95108095; PMID:7809169
A;Accession: I59282
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-788 <RES>
A;Cross-references: UNIPARC:UPI000012DD22; GB:D38448; NID:9643598; PIDN:BAA07480.1; PID:
C;Superfamily: human diacylglycerol kinase; calmodulin repeat homology; protein kinase C
C;Keywords: ATP; calcium binding; duplication; EF hand; phosphotransferase; zinc
F;172-204/Domain: calmodulin repeat homology <EF1>
F;172-249/Domain: calmodulin repeat homology <EF2>
F;269-318/Domain: protein kinase C zinc-binding repeat homology <KZI>
F;334-380/Domain: protein kinase C zinc-binding repeat homology <KZ2>

Query Match 62.1%; Score 38.5; DB 1; Length 788;
Best Local Similarity 61.5%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

Qy 1 CDG---KDYIVLP 10
|||:|||||
Db 380 CDGELKDHILLP 392

RESULT 13

S51100
hypothetical protein 3 - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51100
R;Blasczyk, R.; Wehling, J.; Salama, A.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51099
A;Accession: S51100
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <BLA>
A;Cross-references: UNIPROT:P16190; UNIPARC:UPI0000016AA55; EMBL:X83005; NID:g619869; PID:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 84;
Best Local Similarity 87.5%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 22 DGKDYIAL 29

RESULT 14

I72029
MHC HLA-A3-alpha-2 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I72029
R;Sire, J.; Chimini, G.; Boretto, J.; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, H.
J. Immunol. 140, 2422-2430, 1988
A;Title: Hybrid genes between HLA-A2 and HLA-A3 constructed by in vivo recombination all
A;Reference number: I56009; MUID:88170828; PMID:2450922
A;Accession: I72029
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:Q30177; UNIPARC:UPI0000089D17; GB:M20179; NID:g188495; PIDN:
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:I19310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 89;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 26 DGKDYIAL 33

RESULT 15

I56009
MHC HLA-A2-alpha-2 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56009
R;Sire, J.; Chimini, G.; Boretto, J.; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, H.
J. Immunol. 140, 2422-2430, 1988
A;Title: Hybrid genes between HLA-A2 and HLA-A3 constructed by in vivo recombination all
A;Reference number: I56009; MUID:88170828; PMID:2450922
A;Accession: I56009
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:Q30176; UNIPARC:UPI0000089A2B; GB:M20139; NID:g188493; PIDN:
C;Genetics:

A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 89;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGKDYIVL 9
|||
Db 26 DGKDYIAL 33

Search completed: December 9, 2005, 10:34:37
Job time : 10.5472 secs

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